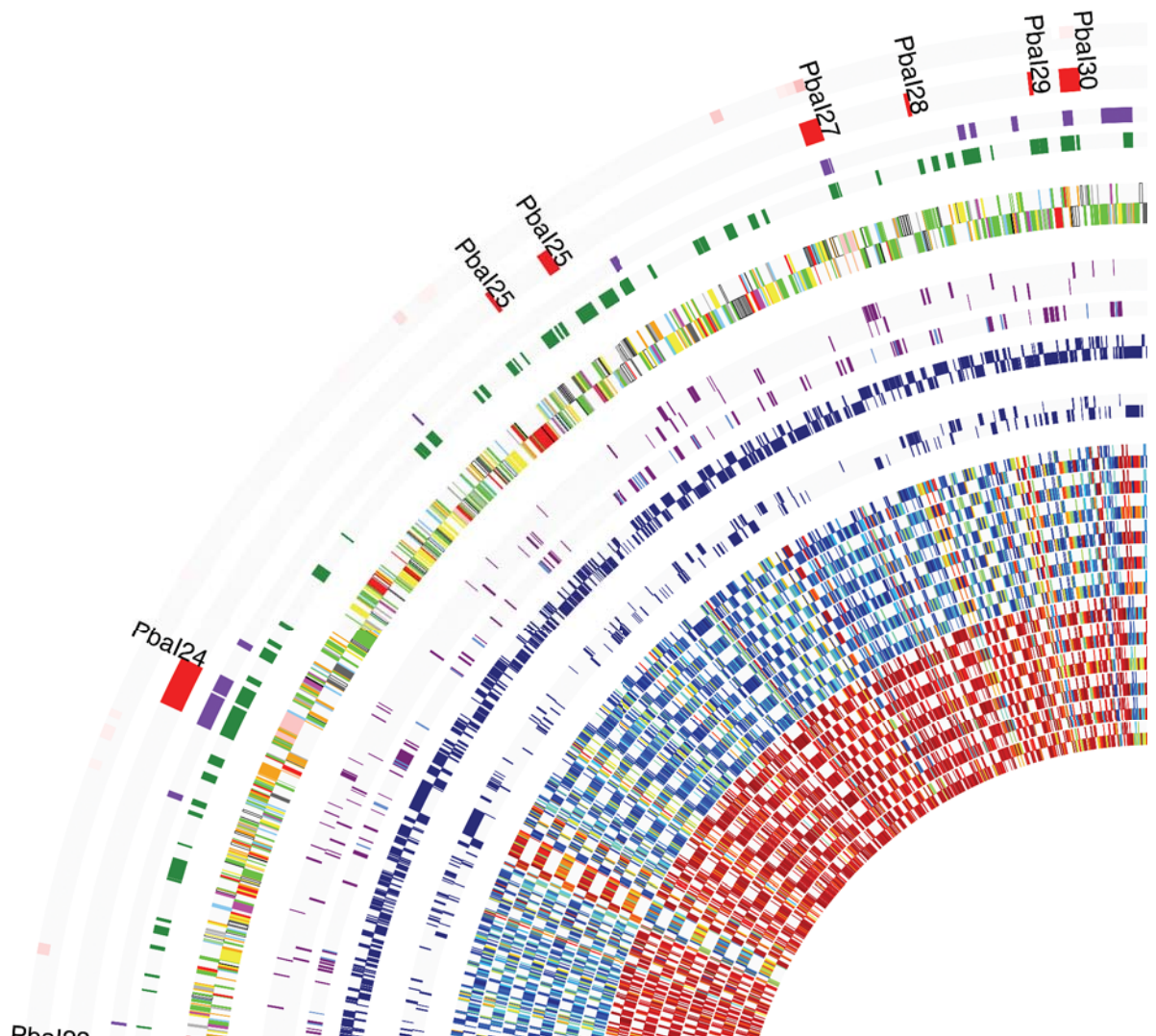


## Annual Report 2007



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# Introduction

**Peter J. Gregory**

What a difference a year makes! After many years in which talk about the production of food crops has been considered by many economists and environmentalists in government as of low priority, the subject is now very much back on the agenda. The diversion of about one quarter of the US maize crop into bioethanol production, coupled with poor harvests in Australia and parts of Asia, increased demand for grain in China and India for meat production and reduced stocks of stored food grains have resulted in substantially higher food prices around the world. Recent articles in the financial press herald the end of an era of cheap food and point out that the political desire for fuel security through increased biofuel production has inevitably linked food prices more closely to that for oil. Moreover, the publication during the year of the Fourth Assessment of the Intergovernmental Panel on Climate Change has focused public attention on a more uncertain future and on the potential effects of various environmental changes on food security especially in the developing world.

SCRI is responding to these challenges in several ways. First, we have increased our research activity of direct relevance to mitigating and adapting to climate change. We have started work on plant mediated transfer of carbon to soils as our contribution to the Scottish Alliance for Geosciences, Environment and Society (SAGES). Our newly created sub-programme on Resource Capture is examining ways to improve water and nutrient use efficiency by crops which will reduce gaseous and leaching losses. Both of these research activities will lead to outcomes that mitigate

climate change. Research on means of adapting to climate change includes work on identifying mechanisms and sources of durable disease resistance, and development of germplasm that has enhanced resistance/resilience to abiotic stresses such as drought and cold funded by our major customer the Rural and Environmental Research and Analysis Division (RERAD) of the Scottish Government.

Another means of both mitigating climate change and adapting to other environmental changes is to develop new crops that will take advantage of more favorable growing conditions in some regions (including eastern Scotland). So, a second change this year has been to refocus parts of our research and develop a programme of Plant Products and Food Quality. This new programme will research the place of non-food crops in Scottish agriculture focusing on plants producing molecules of high value, and also act as a focus for our growing research portfolio on energy crops. A third response has been to build upon our excellent relationship with the University of Dundee to form a joint Division of Plant Sciences containing three joint appointments alongside five university appointments, and to start discussions with several other university schools about a joint research centre with a focus on environmental change and human resilience. These latter discussions are at an early stage but have the potential to significantly enhance the social and policy relevance of SCRI's research while simultaneously examining issues of international significance.

Closer to home, SCRI is delivering to most of



Welcoming Professor Anne Glover, the Scottish Government's Chief Scientific Advisor.

the national aspirations outlined by the Scottish Government. Our contributions to the “Greener” aim are many but particularly noteworthy during 2007 have been the production of a major synthesis of experimental data on cross pollination, seed persistence and movement, and ecological impacts in relation to the introductions of new crops (including GM crops). These outputs from the EU Sigmea project provide the scientific evidence on geneflow underpinning the policies on coexistence of the EU member states. Simultaneously, the EU ECOGEN project, investigating the ecological and economic consequences of GM crops, was successfully completed and published. Highlights of our research contributing to a “Healthier” community include unraveling the complexities of how vitamin C accumulates in fruit and determining the role of bioactive compounds in fruits. We have

demonstrated four potential pathways for vitamin C accumulation in blackcurrant by *in situ* synthesis via the L-galactose pathway, together with the potential for long-distance transport via the phloem. We have also found that polyphenolic compounds in blueberry killed cells of the intestinal parasite *Giardia duodenalis* and increased the encystation of *Cryptosporidium parvum* oocysts. These protozoan parasites are common causes of diarrhea across the world for which there are currently no, or only limited, chemotherapeutic interventions.

Basic and strategic research across the institute contributes to the “Smarter” agenda leading to both knowledge and better practical ways of doing things. We have discovered a translocation signal (the RXLR motif) in virulence proteins of late blight (*Phytophthora infestans*) which facilitates delivery of these proteins





into plant cells and explains how blight establishes itself in potato crops. Interestingly, the finding has broader significance because the signal is also conserved in other, similar pathogens and in distantly related organisms such as the malaria parasite. Through field studies of late blight outbreaks, we have shown that the marked increase in the A2 mating type of *P. infestans* observed across Great Britain in recent years is due to the predominance of a single clonal lineage of the pathogen. This opens the way to a reassessment of current disease management strategies based on host resistance, fungicide application, and minimization of primary inoculum sources.

Improved plant varieties that are resistant to pests and pathogens, use nutrients efficiently and effectively while maintaining or enhancing yield and quality are globally recognized as the most sustainable route to food and environmental security. We have developed a genetic analysis platform for barley that is similar to that used in human genetics and is revolutionizing the way we derive data for genetic analysis. Using an emerging population genetics-based approach termed 'association genetics', we have used this platform to locate versions (alleles) of genes that breeders select for, often inadvertently, within their elite breeding populations. In parallel we have developed software (GERMINATE) that stores, displays and facilitates analysis of this genetic information. With these resources and the forging of a strong and productive collaboration with all of the commercial barley breeders in the UK, we shall develop practical strategies to increase the predictability of plant breeding.

SCRI and Mylnefield Research Services Ltd commissioned DTZ to undertake an assessment of the economic impact of our research. Their market-based survey showed that we contribute £165 million to the UK economy annually representing a 14-fold return on the investment of public money. In addition to the readily quantifiable benefits such as new and superior plant varieties (3 new potato and 1 new raspberry varieties were registered for commercialisation during 2007), there were many other non-quantified benefits such as

those resulting from reduced pesticide applications as a consequence of enhanced disease resistance, and promotion of good land stewardship resulting in less pollution and the protection of soils and landscapes. These contributions to a "Wealthier" community demonstrate the value of institutes such as SCRI in working with businesses with commercial skills that can translate our research into products of value to society.

Our research for RERAD has brought us into daily working contact with the Scottish Agricultural College (SAC). During 2007 we signed an agreement to work more closely together across our shared interests in crop and soil research and knowledge exchange. The first fruits of this closer relationship are evident in joint plans and applications for grants detailed later in this report. Our science strategy places particular emphasis on our international links. During the year we strengthened our relationship with the Norwegian institute BIOFORSK. Scientists from several science programmes (especially Environment-Plant Interactions and Plant Pathology) have good interactions already, but we look forward to closer working on a range of issues common to land use systems in northern latitudes. Our scientific links with institutes in China continue to evolve, and I visited the International Centre for Research in the Dry Areas (ICARDA), Syria to renew our association with a major centre for barley research. We already have funding from the Global Challenge Fund to study the drought resistance and associated genetics of landrace barley, and anticipate a growing level of interaction.

The Director's Award for 2007 went to Phil Taylor for his outstanding contribution in assisting us to communicate our work to diverse audiences. 2008, is the UN Year of the Potato so there will be many opportunities for us to bring our important work to the attention of a wider audience.

I hope that you enjoy reading the details of our current activities in this report.

P J Gregory  
7 January 2008







# Review of events – Highlights

Knowledge transfer is often likened to starting a conversation. 2007 saw many such conversations at SCRI involving a wide variety of scientists, farmers and food industry specialists. We also reached out to thousands of individual members of the public.

SCRI is a LEAF (Linking Environment and Farming) Innovation Centre. The LEAF Open Day on Sunday 10 June was widely publicised in the local community and by mid-afternoon there were 270 cars parked in the grounds and more than 1000 visitors enjoying tractor rides, science displays and hands-on activities in the Living Field and its newly-opened Study Centre.



Professor Geoff Squire with a young student in the Living Field study centre.

SCRI's three, specialist events also thrived in 2007. 'Cereal Solutions', 'Fruit for the Future' and 'Potatoes in Practice' attracted more than 700 visitors – a high proportion of them growers, researchers or industry specialists. 'Potatoes in Practice' continues to draw a high turn-out and is established as the UK's largest potato field event. This year the visitors included producers from Australia, Spain and Egypt.

The guest speaker at 'Potatoes in Practice' was the Director General Environment, Scottish Government, Richard Wakeford. He told his audience that SCRI's



Gaynor McKenzie and Cabinet Secretary Richard Lochhead at the Royal Highland Show.

research on potato genetics and genomics and on potato pathology was at the cutting edge of science in these fields.

SCRI's events team was also active at

- the Gardening Scotland show at Ingliston
- the Six Cities design event in Dundee (with a display on DNA)
- the Dundee Flower and Food Festival
- the Glasgow Science Centre

The Royal Highland Show provided the opportunity for two, very different exhibits of SCRI's research. In the Royal Highland Education Trust pavilion, staff ran a display aimed at youngsters and demonstrating the nutritional qualities of fruit. The RHS also saw the first public appearance of a three metre high, polystyrene mountain! It was the brainchild of Gavin Ramsay and Gaynor McKenzie of the Commonwealth Potato Collection. It demonstrated to great effect the origins of the potato in the high peaks of the South American Andes.

SCRI was host to a wide range of official visits during the year. The Scottish Government's Chief Scientific Adviser, Professor Anne Glover, visited in May; three separate,



Andrew Welsh MSP (left) and Peter Gregory at the summer reception.

Chinese government delegations came for briefings including one led by the vice Minister for agriculture, Zhu Baocheng; and an evening reception and buffet supper in August, hosted by the Director, had a guest list including John Purvis MEP, Andrew Welsh MSP, Alex Johnstone MSP, and Provost John Hulbert JP of Perth and Kinross Council.

There were individual honours and successes for SCRI members of staff during 2007. Michael Ravensdale and Rene Sonnenberg, PhD research students with SCRI, were both finalists in the 2007 SABRI/SAC postgraduate competition. Both were introduced to HRH The Princess Royal during the presentation ceremony at the Moredun Research Institute.



Visit by the Chinese Vice Minister of Agriculture, Zhu Baocheng.

An event of great significance for SCRI was the signing on 29 May of a memorandum of understanding with the Scottish Agricultural College. Particular areas

for collaboration include crop disease and pest management, soils and the science and economics of sustainable agriculture. The two organisations are also sharing the job of passing knowledge on to the farming and food industries, schools and the public.

Dr Tim George of Environment Plant Interactions was awarded a Royal Society of Edinburgh Fellowship to pursue his work on the resilience of Scottish agriculture in the face of global environmental change. Dr Derek Stewart, the head of Plant Products and Food Quality, was made a Fellow of the Royal Society of Chemistry. Rex Brennan was awarded the Scottish Horticultural Medal for his work as leader of the Soft Fruit Genetics & Pathology work programme.

SCRI's strength as a research centre comes from its individual members of staff. Their dedication over many years was officially recognised in October when forty scientists and support staff received long service awards.



On the same day, SCRI bade farewell to Keith Hopkins, who stood down from the Governing Board after ten years' service.





# Genetics

**Robbie Waugh**

*Developing a framework that improves our ability to characterize, interpret and manipulate the allelic diversity that exists within crop plants underpins ongoing increases in global agricultural productivity, and forms the core of the Genetics research program.*

Several barley projects have focused on using a high throughput molecular marker platform based on *Illumina's* Oligo Pool Assay (OPA). Bill Thomas, Luke Ramsay, Joanne Russell and Andy Flavell (Division of Plant Sciences – DoPS) have assembled extensive collections of barley germplasm that include cultivars, globally distributed landraces and wild collections. As well as characterizing the extent and distribution of genetic diversity in these collections, they have been exploring whether the approach termed ‘association mapping’ can be successfully applied to locate the genes controlling a range of phenotypes (see article by Joanne Russell and colleagues). The genetic information revealed by the OPA, combined with historical and newly assembled phenotypic data, has enabled them to identify regions of the genome that have been selected during genetic improvement of both monogenic and polygenic traits including yield and malting quality. For example, in European spring barley they have recently identified allelic changes at multiple loci selected for during the breeding progression from the highly

successful landmark cv. Triumph to the cv. Westminster (first recommended in the UK in 1980 and 2005 respectively), covering an improvement of over 3% in hot water extract. Given these successes we intend to develop OPA's for both potatoes and soft fruits.

In potato, Glenn Bryan's group has performed further detailed characterisation of the late blight resistance found in the cultivar Stirling, leading to the identification of a number of candidate genes for a large effect resistance QTL on chromosome IV. John Bradshaw and colleagues have extended genetic analysis of a tetraploid potato population derived from a cross between the processing clone 12601ab1 and cv. Stirling to include yield, agronomic and quality traits routinely measured in breeding programmes. Their analysis used improved genetic analysis software developed by Christine Hackett and Iain Milne of BioSS called ‘TetraploidMap for Windows’. Linked molecular markers provide an opportunity for the breeder to use molecular breeding (gene cloning and marker-assisted selection) to ensure that beneficial combinations of





genes and alleles are introduced into new cultivars as quickly as possible. These approaches will supplement the traditional ways of exploiting genetic variation in potato breeding programmes, which – even when incorporating new technologies – will continue to rely on classical quantitative genetics, highly mechanized field-work and computer-based data capture and analyses for genetic gain.

Genetic analysis of *Rubus* (raspberries) and *Ribes* (blackcurrants), led by Julie Graham and Rex Brennan respectively, has identified genetic markers linked to Phytophthora root rot (*Rubus*) and gall mite (*Ribes*). The region around the raspberry *H* gene, linked to resistance to cane Botrytis and spur blight, has been saturated with new markers. The potential utility of these as tools for indirect selection is currently being explored in the MyInfield Research Services soft fruit breeding programme to supplement an enterprise that last year released several new commercial cultivars including Glen Fyne (raspberry), and Ben Starav and Ben Klibreck (blackcurrant).

Joanne Russell has driven the application of genomic tools to species of high conservation priority. Understanding the reproductive mode of the endangered sub-arctic willow scrub, which typically occurs on steep crags in Scotland, is important both for the design of restoration programmes and for land management decisions (e.g. grazing) that may impact population survival. An analysis of the reproductive strategy in the largest UK stand of sub-arctic willow scrub revealed little evidence for clonal growth, most individuals possessing distinct multi-locus genotypes. These results suggest that material for reintroduction should be sexually (rather than clonally) derived. Similar genetic approaches are being used to inform development of strategies for the conservation and restoration of fragmented populations of Scots pine and their associated ground flora and for tropical species such as *Allanblackia*.

Last year we significantly expanded our research on 'extreme phenotypes' of barley. Frequently the result of chemically or physically induced mutations, they comprise a new focus for the barley program which

is also enhancing interactions with DoPS (and other universities). Individual mutants altered in inflorescence development, leaf and root morphology and the fundamental process of recombination have been entered into an intensive crossing programme to develop segregating populations required for positional cloning. Investigating fundamental aspects of grain development, genes responsible for grain shape are being sought by David Leader and Arnis Druka. In collaboration with Claire Halpin (DoPS), mutants have been identified that have altered lignin content, and these are being investigated for their potential as increased digestibility feedstocks and for bio-energy production. As they potentially impact plant development, yield and quality, inflorescence mutants are being investigated in collaboration with Dr. Gordon Simpson (DoPS).

While variation in the protein coding sequences of structural genes is commonly associated with functional biological diversity, it has recently become clear that regulation of gene expression is central to variation in specific biological processes. Current estimates suggest that at least 35% of plant genes undergo alternative splicing, a regulatory process that increases protein diversity and modulates expression levels. The RNA group led by John Brown and Craig Simpson has developed a system to accurately and reproducibly measure changes in alternative splicing of multiple genes simultaneously. Their technology is currently being used in *Arabidopsis* to study the responses of genes to stress such as temperature (cold, heat) as well as in mutants of genes involved in splicing regulation and flowering time. Similar studies are being planned in barley.

Changes in the flowering time of many plant species in Britain has provided some of the best biological evidence for climate change. However, we know relatively little about how plants perceive and respond to modest changes in ambient temperature. The intricacy of gene regulation in flowering time control is probably the best-studied example of post-transcriptional regulation of plant development. Gordon Simpson's group has successfully developed a method for cross-linking RNA binding proteins to their target RNAs *in vivo* as a means to reveal the mechanisms that underpin post-transcriptional control. They are currently studying how changes





The December 2007 meeting at SCRI of the Barley Breeders Network.

in RNA processing may mediate responses to different ambient temperatures.

The *DNA Sequencing and Microarray Facility* operates across the scientific programmes under the leadership of Pete Hedley. Last year it ran over 120K sequencing / genotyping runs for projects covering: the identification of pathogenicity determinants during potato soft rot (*Pectobacterium*) infection; disease response mechanisms in crop species; quality trait (flavour and texture) dissection in potato tubers; resistance to *Phytophthora infestans*; and the regulation of somatic embryogenesis in potato (see article by Glenn Bryan and colleagues). Microarray technology is being used to identify key changes in gene expression associated with dormancy break in blackcurrants, which relates directly to the negative impact of climate change on budbreak. A pioneering study examining the genetics of variation in mRNA transcript abundance is described in the article by Arnis Druka and others.

With such complex and large datasets (last year we collected over 12M genotypic datapoints for barley alone) we rely increasingly on appropriate bioinformatics and statistical tools to store, analyse and display our results. The GERMINATE database and associated tools developed by the Bioinformatics group led by David Marshall (and Andy Flavell (DoPS)) has been adapted and optimised to handle genotype data

from the OPA platform. GERMINATE can handle data sets with an excess of 30,000 plot records for a single trait. Current developments include a graphical interface that enables users to visualise data summaries directly from database queries. Of particular practical importance has been the visualisation of genotype data either directly from the database through the web interface or on larger scale using the Java-based Genotype Visualisation Tool (GVT) that enables users to compare, sort or cluster high resolution graphical genotypes from a large number of plant lines.

Comparative genetic analysis has also received significant attention. The development of the “Relator” application is attracting considerable interest from scientists involved in sequence based genomics technologies such as microarray analysis.

Many of the highlights listed above rely on the abilities of my colleagues to win funding in a highly competitive environment. Last year they redoubled their efforts, and their considerable success has guaranteed that Genetics will maintain a vibrant research portfolio extending well past 2010. Perhaps the most significant impact has come from the increasingly productive interactions with DoPS. I am indebted to the continual energy, enthusiasm and abilities of my colleagues, and look forward to a productive 2008.



# Drought tolerance in Mediterranean barley: An association genetics approach

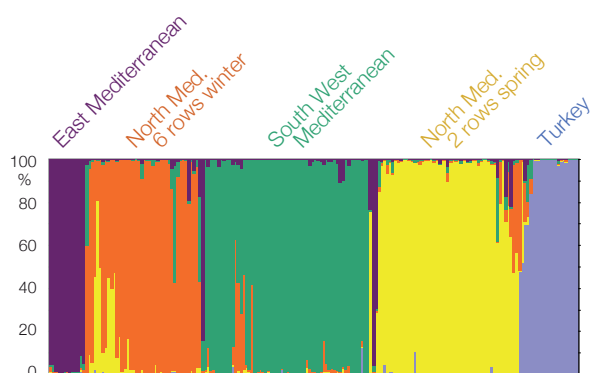
**Jordi Comadran, Ignacio Romagosa, Fred van Eeuwijk, Christine Hackett, Joanne Russell and Bill Thomas**

The Mediterranean region from the Maghreb to the Near East is characterised by strong water deficits and often suffers from strong drought events.

The region has one of the fastest growing food deficit records in the world and could face catastrophe if their remaining natural resources are not properly managed and conserved. This makes drought management and mitigation a high priority in these countries. Barley is one of the most reliable crops in the Mediterranean region, grown in a wide range of conditions, particularly in marginal environments, often at the fringes of deserts and steppes, receiving modest or no inputs, by resource poor farmers. In order to sustain significant genetic gains for drought areas, a deep understanding of the basic underlying physiological mechanisms of adaptation to drought, resulting in improved water use

efficiency, is required. Conventional breeding and high yielding varieties have had virtually no success in the poorest sites in this area. But this lack of success has had a positive effect in preserving biodiversity because in these environments all the barley grown is landraces, which have evolved directly from the wild progenitor in hostile environments, providing a rich reservoir of genes for adaptation and survival to the harsh natural environment (for a review of barley landraces see Grando *et al.* 2001). By tapping into this natural diversity and combining these with a range of analytical approaches, we have identified QTLs that are genuinely associated with yield in stressed environments.

As part of an EU INCO-MED funded project entitled 'Mapping Adaptation of Barley to Drought Environments (MABDE), we have compiled a database of extensive genotypic and phenotypic measurements and developed appropriate statistical methods for assessing marker-trait associations to understand the genetic and physiological dynamics underlying barley domestication and intensive breeding carried out in the last century in relation to adaptation to drought. A diverse collection of 192 barley genotypes (DBG) (83 landraces, 43 old cultivars and 66 new cultivars) selected to represent key agro-ecological regions from all around the Mediterranean Basin together with relevant genotypes from the rest of Europe has been assembled. A particularly important feature of this collection is the inclusion of the Central and Northern European types as this reflects the breeding development of barley in which germplasm flowed from the Fertile Crescent to ultimately give rise to contemporary cultivars in these regions. Population structure and genome-wide linkage disequilibrium (LD) were investigated using 52 nuclear microsatellite and 1131 DArT® markers. Both clustering and coordinate analyses clearly subdivided the sample into five distinct groups clustering around key ancestors and regions of origin of the germplasm, revealing that individuals closely correspond to the geographic regions in which they were grown (Figure 1). In highly structured samples like the DBG, accounting for population structure in association mapping studies is essential and the persistence of LD that was detected meant that association mapping could be used to locate QTLs. The



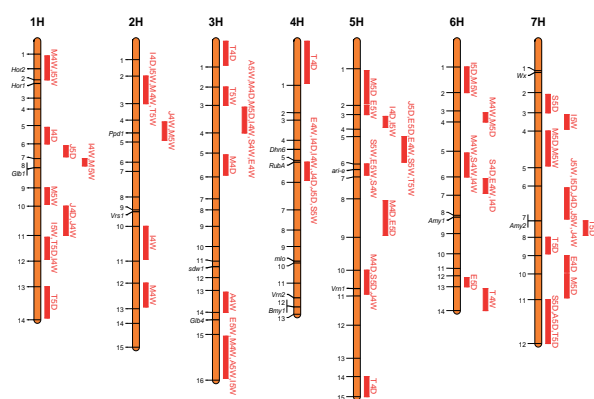
**Figure 1** Inferred population structure based on 192 individuals and 50 markers using STRUCTURE (Pritchard *et al.*, 2000a). Each individual is represented by a line partitioned in k coloured segments that represent the individual's estimated membership fractions in K cluster.





population was phenotyped and yield data collected from 28 field trials grown across seven countries, using sites with contrasting water status in each (either by irrigation or utilising past history), over 2 years. The yields observed for individual genotypes ranged from 10t/ha to complete failure of individual genotypes to produce any seed whatsoever due to the stress. The multi-environment QTLs detected in the DBG, were found most frequently in bins 4, 6, 6 and 7 on barley chromosomes

3H, 4H, 5H and 7H respectively (Figure 2) and with the exception of bin 4 on chromosome 3H, can be substantiated by results from other relevant studies in barley. One of the encouraging findings in the present study is the detection of significant genetic variation for yield in the eight severely stressed environments where the mean yield was less than 2t/ha, and one of the most consistent genomic regions was in bin 7 on chromosome 7H, where four out of the five significant associations came from the Jordanian sites with mean yield ranging from 0.3 to 1.2 t/ha.



**Figure 2** Barley bin map showing significant associations with yield.

This association mapping population is genetically and physiologically diverse, strongly structured based on the pedigrees providing contrasting levels of population stratification. Current genome coverage, together with observed LD decay values, should not present problems for attempting a whole genome scan and makes the population an ideal QTL mapping resource for the Mediterranean environmental conditions provided that population structure is effectively and appropriately controlled within the association analysis.

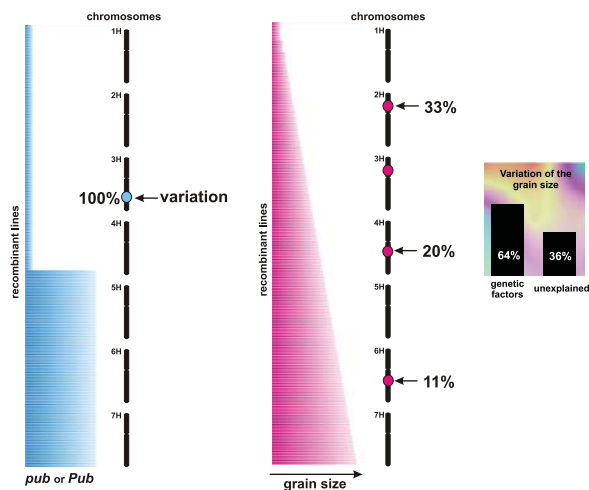


# The genetics of gene expression

**Arnis Druka, Elena Potokina\*, Mike Kearsey\*,  
Zewei Luo\* and Robbie Waugh**

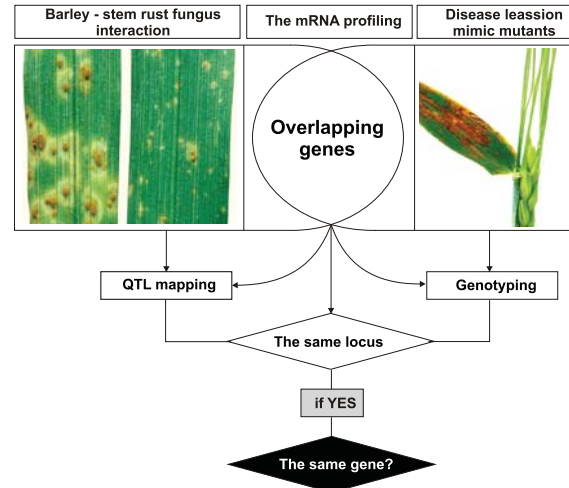
**\*University of Birmingham**

Most important plant characteristics, such as grain quality or yield, are controlled by many genes and influenced by the environment. In plant breeding and genetics these are usually monitored in defined populations by recording a score for that characteristic on a sliding scale. Such measurements are both subjective and often distantly removed from the biological processes giving rise to them (e.g. yield). Environmental and other factors may also impart significant additional variation. The resulting imprecision restricts our ability to identify the location of the genes controlling the characteristic and the overall approach provides no information at all about the complex network of genes or gene-products which are responsible for determining why the measured phenotype is at one extreme or the other. Advances in molecular biology



**Figure 1** Phenotypic variation of Mendelian or binary traits can easily be explained by a single gene or locus. This contrasts with quantitative traits, where genetics behind phenotypic variation often is quite complex and usually not all of it can be attributed to the genetic factors. *Pub* and *pub* shown here as an example, are alleles of the unknown gene, that determine presence or absence of the hairs on the leaves. Such Mendelian or binary trait can easily be converted to the quantitative trait if number of hairs per individual line is counted.

have made it possible to measure the abundance of thousands of gene products, known as transcripts, in a single experiment by using an approach termed 'microarray technology'. For example, in barley we use a microarray that measures the abundance of 23,000 different transcripts in a single experiment. The overall profile of variation in transcript abundance obtained from such an experiment represents a snap-shot of the important biological processes that are operating in the material being studied at the time of sampling. By correlation with classical trait scores it has been shown that transcript abundance can serve as a 'surrogate' (i.e. an indirect measurement) for classically recorded characters. For example, variation in transcript abundance has been used to identify 'susceptibility loci' for complex diseases like obesity, asthma and diabetes in mammals, and the overall approach is now being used to differentiate between healthy and different forms of cancerous cells.



**Figure 2** The strategy we use to identify candidate genes for complex traits. Three different components are employed; experimental population where the trait segregates, induced mutations-containing lines, that either have obvious phenotype related to that of segregating population (forward genetics approach), or mutations in the candidate genes (reverse genetics, TILLING). As a third component, mRNA abundance phenotypes of thousands of genes are used to link the first two.

In this example, we specifically address group of PCD-related genes that have eQTLs associated with those of partial resistance to the wheat stem rust fungus in barley. We also mapped the phenotype of one of the disease lesion mimic mutants to the same locus.

We quantified the relative abundance of 23,000 different transcripts in two different barley tissues from each of the individuals in a segregating population that has also been analysed for a wide range of classical phenotypic traits. We wanted to determine whether, like the mammalian studies, we could identify the major genetic determinants underlying classical characteristics while at the same time gain biological understanding of the networks of gene-products that underly their development. In our experiment, 12,738 of the barley genes on the chip recorded variation in transcript abundance that segregated in the population. By using standard genetic mapping approaches we were able to show that over a third of these 'transcript abundance' phenotypes behaved as single genes and as a result we were able to construct a high density map of the barley genome with each of the genes ordered along each

of the chromosomes. We then performed correlation analysis with classically scored phenotype from the well studied interaction between barley and the wheat stem rust fungus *Puccinia graminis f. sp. t ritici* as a model. We showed that the approach successfully predicted the *Rpg1* resistance gene as a major contributor to resistance and highlighted several other candidate genes and loci that contribute to this interaction. We are now performing a detailed experimental analysis of one of the loci we identified and named Required for Puccinia resistance 2 (*Rpr2*) that putatively encodes a 'master regulator' of a process called programmed cell death. To allow both ourselves and remote users to investigate further correlations within the dataset to additional phenotypic traits we have deposited all the information in an online data analysis environment called the GeneNetwork (<http://www.genenetwork.org/>)





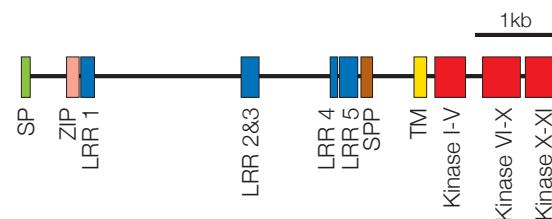
# Somatic embryogenesis in potato

**Sanjeev Kumar Sharma, Steve Millam, Pete Hedley, Ingo Hein, Jim McNicol & Glenn Bryan**

Potato, the world fourth most important food crop, is largely propagated via tubers from the previous crop. Tissue culture techniques, mainly micropropagation, have substantially augmented the supply of potato planting material, the demand for which is rapidly rising, driven by increasing markets in China and India and the development of specialist cultivars for the home market. Micropropagation can reduce the time required for the release of new cultivars from more than a decade to as little as three years and has a vital role in any plant breeding programme in the rapid bulking of advanced breeding material. Clonal *in vitro* propagation methods not only maintain crop uniformity, but also preserve health status as the planting material has reduced exposure to soil-borne and other diseases, principally viruses. We have recently developed an efficient somatic embryogenesis (SE) system for potato (Sharma & Millam 2004), which has considerable promise for rapid propagation of potato material. In this process tissue culture material is used to induce the formation of embryonic structures from callus tissue, by a series of manipulations of the growth conditions.

Despite the advantage of rapid propagation (up to 40 times faster in the early stages than micropropagation) one concern about SE, and indeed all clonal propagation methods, relates to the level of genetic stability of the material generated. It is of fundamental importance that micropropagated plants, irrespective of their development through either organogenesis or embryogenesis, remain 'true-to-parental' type. Potato is known to be subject to low levels of somaclonal variation, which can be due to both genetic and epigenetic causes. In our studies, Desiree plants obtained through different propagation routes (SE, axillary bud proliferation, microtubers) were evaluated

for somaclonal variation using phenotypic, cytological and molecular (amplified fragment length polymorphism, AFLP) approaches. In our study, no phenotypic or cytological differences were observed. However, low levels of AFLP variation were seen for SE (0.66% bands polymorphic) and microtuber grown plants (0.44%), and intriguingly, this variation was only observed when AFLPs were performed using methylation sensitive restriction enzymes. This suggests a possible role for methylation in the generation of somaclonal variation,



**Figure 1 a.** Photograph of germinating potato somatic embryo contained in sodium alginate bead.

**b.** Generalized structure of StSERK1, 'SP' denotes signal peptide, 'ZIP' Zip domain, 'LRR' Leucine Rich Repeats, 'SPP' Proline rich domain containing SPP (Ser-Pro-Pro) motif, 'TM' alanine-rich hydrophobic trans-membrane domain, 'Kinase' serine-threonine kinase domains.





although further detailed studies are required to investigate this phenomenon.

Another goal of our research has been to gain a better understanding of the molecular events taking place during SE. A primary objective has been the isolation of a potato orthologue of a class of gene known to play an important role in SE in other plants, such as *Arabidopsis*. We have cloned and characterised a *SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE* (*SERK*) gene from potato, using a range of molecular approaches. *SERK* genes have been shown to mark and enhance embryogenic competence in somatic cells of model plant species. Sequence analysis of *StSERK1* reveals very high levels of similarity to other plant *SERKs*, as well as a conserved intron/exon structure which is unique to members of this family. Monitoring of *StSERK1* expression during the progression of potato SE revealed increased expression during the 'induction' phase of SE, and we also observed up-regulation of *StSERK1* expression in somatic embryos. We believe that the *SERK* gene family may serve as a marker of

tissue pluripotency, rather than embryogenesis in the strict sense (for further details see Sharma et al., 2008). A second elucidatory approach has been to monitor global gene expression changes during SE using a 10K spotted potato microarray developed at The Institute for Genomic Research (TIGR). Analysis of these data, still in progress, has identified a number of genes implicated in the molecular changes occurring during the establishment of SE, as well as several parallels with other plant SE systems. This integrated study is the first of its kind in potato embryogenesis and offers information for potential uptake in a wide range of crop improvement and basic research programmes.

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# Plant Pathology

**Lesley Torrance**

*Work in the Plant Pathology Programme has continued to exploit pathogen genomics and comparative genomics resources to advance our research. This approach has been highly fruitful in shaping new hypotheses to address basic research questions and emerging issues of substantial importance to science policy.*

A new area of research on the survival of human enterobacteria on plants was established with the appointment of Dr Nicola Holden. Contamination of leafy vegetables and other plants by human enterobacteria such as *Escherichia coli* O157:H7 and *Salmonella typhimurium* is becoming more frequent and evidence is accumulating that these pathogens can persist in association with plants posing considerable risks to human health. Within the PP programme, comparative genomics of enterobacterial pathogens of plants such as *Pectobacterium atrosepticum* (causing black leg of potato) has been a highly productive source of new information leading to new hypotheses of how human enterobacteria bacteria may survive on plants, for example, through horizontally-acquired islands of genes that are transferred between species. Dr Holden will help to help drive forward studies to investigate the adaptation of bacteria to different environments to address this problem.

We continue to attract competitive research income to extend and add value to our research and notable grants awarded this year include Paul Birch and colleagues who were successful in obtaining £536,000 grant from the BBSRC Crop Science Initiative to exploit the *Phytophthora* genome sequence for novel targets for potato resistance. In addition, SCRI nematologists are members of the consortium that has secured funding from BBSRC to sequence the genome of *Globodera pallida* at the Wellcome Trust Sanger Institute – opening the door to apply modern genomics technologies to control this important nematode pathogen of potatoes.

During the year Paul Birch was appointed to a personal chair in Plant Pathology equally funded by the University of Dundee and SCRI. John Jones was appointed Guest Professor at The University of Ghent, Belgium and is Chair of EU Cost Action 872 'Exploiting genomics to understand plant–nematode interactions'



In December, an external peer review was conducted to assess the Quality of Science produced by the programme; this included presentations, review of publications and individual interviews. Overall, the report was positive and highly complimentary with the review team concluding that PP research is predominantly of an internationally competitive standard with high strategic value to Scottish agriculture and the UK economy. The review involved a substantial amount of work by our administrative assistant Lesley Young in the preparation of documents. I would like to take this opportunity to thank the review team and Lesley Young for their work on our behalf.

#### Research Highlights include:

Work in the *Phytophthora infestans* group led by Paul Birch and Steve Whisson has discovered a translocation signal in virulence proteins from *P. infestans* (the cause of late blight disease), that is required for delivery of these proteins into the plant cell. This finding advances our knowledge of how the late blight pathogen can establish infection in potato cells. The finding has broad significance because the signal is also conserved among other oomycete pathogens and distantly related organisms such as the malaria parasite (Whisson et al., 2007, Nature 450, 115).

In work funded by the BPC, David Cooke, Alison Lees and colleagues have conducted a detailed survey of *P. infestans* from disease outbreaks in GB potato crops. This showed a marked increase of the A2 mating type of the pathogen with most of the change being due to a single clonal lineage. Work is now underway to examine the implications of this change to the effectiveness of current disease management strategies based on host resistance, fungicide application and minimisation of primary inoculum sources.

Genomics technologies have been instrumental to Ian Toth and colleagues in the bacteriology group in identifying key virulence factors involved in the later stages of potato infection by *Pectobacterium*. We now know that factors involved in manipulating potato resistance inside plant cells are produced at the same time as plant cell wall degrading enzymes, which attack the plant cells from the outside. This dual factor attack may be

necessary for a successful infection and offers further targets for control. A transcriptomics approach linked to plant pathogenicity testing has been used to determine the complete quorum sensing regulon of *Pectobacterium*, linking many known and putative virulence determinants to this master regulator of pathogenesis.

Strategic research on plant caspases has led to novel findings showing that the *Agrobacterium tumefaciens*-encoded VirD2 protein (a key element in *Agrobacterium*-mediated plant transformation) is a genuine target for plant caspase fragmentation. These findings have allowed Misha Taliansky and his colleagues to develop novel platform technology for *Agrobacterium*-mediated gene transfer (plant transformation) based on a protection of the VirD2 protein from caspases (Reavy et al., 2007 Plant Cell Reports 26, 1215). In addition, the Taliansky group research on virus movement has revealed novel interactions between virus movement proteins and plant nucleolar proteins called Cajal Bodies. The groundnut rosette virus ORF3 interacts with fibrillarin (a component of Cajal Bodies) and studies showed that this interaction was essential for systemic infection of plants (Kim et al., 2007, PNAS 104, 11115; Kim et al., 2007, EMBO J 26, 2169).

In collaboration with John Carr at the University of Cambridge, Peter Palukaitis and colleagues found that the 2b gene of a severe strain of cucumber mosaic virus caused developmental virus-like symptoms when expressed transgenically in *Arabidopsis thaliana*, while the 2b genes of mild strains did not. The effects on development correlated with inhibition of microRNA (miRNA) turnover, but not on suppression of small interfering RNA (siRNA)-mediated RNA silencing, which occurred with all three 2b genes tested. Thus, the induction of symptoms is not necessarily a direct consequence of RNA silencing suppression. The Palukaitis group also investigated whether transgenic plants that express genes under the control of the cauliflower mosaic virus (CaMV) 35S RNA promoter would facilitate recombination of the CaMV viral genome into plant genomes. Four plant species (tobacco, oilseed rape, *A. thaliana* and *Nicotiana benthamiana*) were investigated and the data obtained do not support this hypothesis. Moreover, transgenic plants containing a 35S RNA





Dr David Cooke at work in a potato plot at SCRI

promoter also did not facilitate the seed transmission of CaMV from infected plants to their progeny. In addition, it was shown that infection of transgenic plants of the same four species by a mild CaMV strain did not suppress expression of the transgene or affect the stability of the transgene. In combination with other reports, this work shows that CaMV infection leading to suppression of the expression of transgenes driven by the CaMV 35S RNA promoter is highly dependent on both the host and the virus strain combination.

Work on potato mop-top virus (PMTV) movement in collaboration with Dr Eugene Savenkov on sabbatical leave from the Swedish University of Agricultural Sciences has revealed a number of novel findings including the rod-shaped particles of PMTV appear to be polar and contain the coat protein readthrough

domain and TGB1 movement protein at one extremity, and that this association is essential for long distance movement of virions. The role of movement protein TGB2 was examined and in addition to its known association with cellular membranes in the secretory and endocytic pathways to facilitate movement it also targeted chloroplasts to facilitate virus replication and/or pathogenicity. We found specific interactions between TGB2 and lipids important in signal transduction and lipid raft formation, suggesting that TGB2 plays key roles at different stages of the virus 'life cycle'.

The three accompanying articles feature research findings on new viruses in raspberries; analysis of EST sequences from cDNA libraries of the virus vector aphid *Myzus persicae* and analysis of over 4000 *Globodera pallida* ESTs from two life stages that has revealed novel secreted proteins.

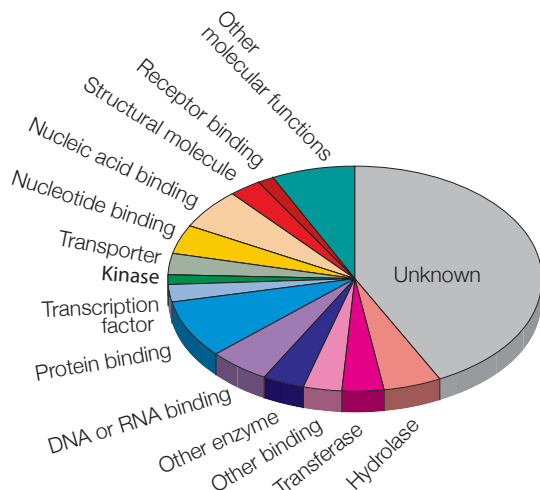


# Aphids join the genomics age

**Brian Fenton, Gaynor Malloch, Agnese Winfield, Alex Wilson<sup>1</sup>, John Ramsey<sup>2</sup> & Georg Jander<sup>2</sup>**

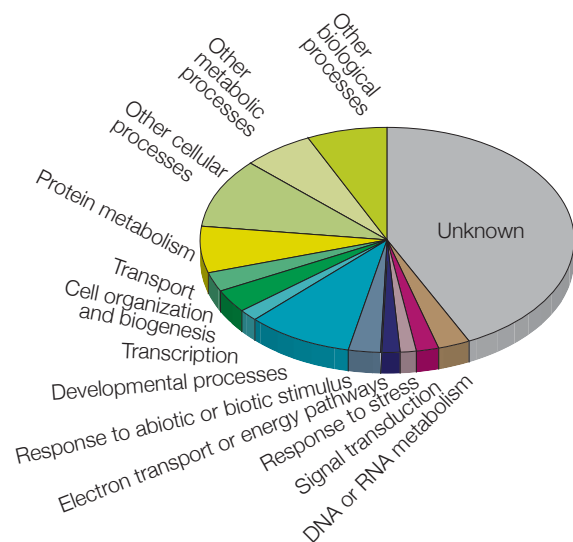
<sup>1</sup>Department of Biology, University of Miami, Coral Gables, Florida 33146, USA; <sup>2</sup>Boyce Thompson Institute for Plant Research, Tower Road, Ithaca, NY 14853, USA

In recognition of their importance as plant pests, a group of international scientists, including a representative from SCRI, met in Paris, France, 2003 under the banner of starting AGIN (aphid genomic international network). These scientists shared an interest in the analysis of aphid genomes and were gathered to decide which aphid species should be the subject of a genome sequencing project. The vote was close, but the pea aphid (*Acyrtosiphon pisum*) won, with the peach potato aphid or green peach aphid (*M. persicae*), SCRI's choice, a close second. *M. persicae* is considered the main vector which spreads viruses within the Scottish seed potato crop. The sequencing of pea aphid genome is now complete and annotation is underway. While the pea aphid exhibits genome differences these are minor, and many genes have high identity and a presumed similarity in function to *M. persicae* genes. The Paris meeting also forged new alliances, and from this developed cooperation between SCRI and Cornell



**Figure 1** Distribution of Gene Ontology biological process annotations, compared between non-normalized libraries.

University in the production of expressed sequence tags (ESTs) for *M. persicae*. This cooperation has led to a publication (Ramsey *et al.* 2007) and production of a *M. persicae* microarray. The output from aphid EST analysis has already identified challenges for the immediate future. The joint *M. persicae* EST analysis produced ~27,000 ESTs, which is an awful lot of information, and analysis has required the use of bioinformatics, a combination of computing power and software expertise. Using bioinformatics it is possible to search databases for similarities to genes from other insects and these similarities allocate an EST to a functional class, based on their known involvement in biological processes or molecular functions (GO – gene ontology). Another insect, *Drosophila melanogaster*, the genetically well known fruitfly, is used as the comparator. Figures



**Figure 2** Distribution of Gene Ontology molecular function annotations, compared between non-normalized libraries.

1 and 2 are diagrams using data generated from an analysis of the collection of *M. persicae* ESTs using the GO method. While many of the sequences could be matched to a *Drosophila* protein with a known function, it was clear that almost half had no known match and were labelled as 'orphans'. An EST analysis of the pea aphid also discovered that 59% of the sequences identified in their study had no known equivalent (Sabater-Muñoz *et al.* 2006). Only half the ESTs cross correlated between the two studies, and this means that there are





probably many more unique aphid genes that will only be identified on the completion of the aphid genome project. It is possible that the figures represent slight overestimates of the true number of unknown genes, but it is already clear that many do correspond to coding sequences where the protein products have an as yet unknown function. These 'orphan' sequences represent completely unknown proteins involved in as yet uncharacterised biochemical or biological processes. Aphids manipulate plants in a variety of ways and the potential for discovering genes with potential use in biotechnological applications is high.

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# Potato cyst nematode genomics

John T. Jones, Mark S. Phillips & Vivian C. Blok

The potato cyst nematodes (PCN) cause damage valued at £50 million in the UK each year. The white species of PCN, *Globodera pallida* causes particular problems to farmers as there are few commercially viable cultivars that have high levels of resistance against it. Problems caused by *G. pallida* are not limited to the UK; this pathogen is spreading across the EU and has recently been discovered in the Ukraine and Idaho, two of the largest potato growing regions in the world. In a completely novel approach, the genome of *G. pallida* is being sequenced in order to help the search for novel control strategies against this pathogen.

The genome sequencing project, a £1.7 million BBSRC-funded grant, will be run by a consortium consisting of SCRI, Leeds University, Rothamsted Research and the Wellcome Trust Sanger Institute. The sequence will emerge over the next three years and bioinformatic analysis and annotation will allow all the genes present in the nematode to be identified. Each of the partners in the project will use the information from the genome sequence to underpin functional studies on various aspects of the biology of *G. pallida*. At SCRI the focus

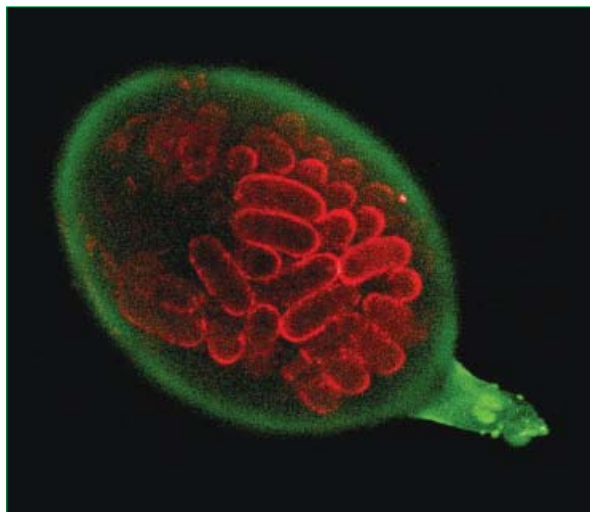


Figure 1 A cyst of *G. pallida* (green) with eggs (red) containing the next generation of juvenile nematodes.

will be on understanding how the nematode invades plants and establishes the complex feeding structures that provide it with the nutrients required for development to the adult stage. Understanding how the host plant recognises the nematode in a resistant interaction will be another important area for future studies.

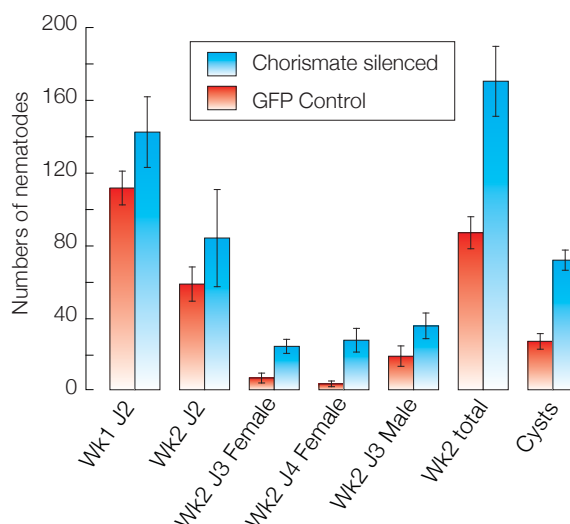


Figure 2 Numbers of nematodes developing on plants after exposure to double stranded RNA targeting chorismate mutase (red bars) or a control gene (GFP - blue bars).

The identification and functional characterisation of proteins secreted from nematode gland cells into the plant is of key importance to both these areas. Much of our previous work in this area has focused on characterisation of a secreted chorismate mutase which is thought to be important in plant–nematode interactions. Silencing this gene using RNA interference reduces the ability of the nematodes to infect plants (Figure 2) and the effect is most pronounced on nematodes that develop into adult females. This is important as sex is determined by food source in *G. pallida*; nematodes that develop on a large healthy feeding site can become female while those that obtain less food become male. This implies that the chorismate mutase either helps induce the formation of the feeding site or that it protects it from defence responses of the host. The latter possibility is currently being investigated in more detail. The genome sequence of *G. pallida* will revolutionise work in this area, providing a full list of candidate genes that may play a role in the parasitic process that can be fed into functional testing programmes.



Genome sequencing is now underway for two other plant parasitic nematodes as well other nematodes that parasitise humans or that are of veterinary importance. The availability of these sequences and the *G. pallida* sequence will allow comparative studies that will reveal the evolutionary relationships of these nematodes and that will shed light on what is required to become a parasite of an animal or of a plant.

Although there will be numerous scientific benefits from this project, the main goal is to provide novel

strategies for the sustainable management of PCN. Information from the project will help identify new genes or nematode-specific enzyme pathways that can serve as targets for novel nematicides. The project will help develop a better understanding of interactions of PCN with its natural enemies that will aid identification and development of effective biocontrol isolates. Finally, improved pest management tools will come from a better understanding of biologically important phenomena such as dormancy and virulence characteristics.





# Discovering new viruses in raspberry crops

**Stuart MacFarlane, Wendy McGavin and Alison Dolan**

Although great care is taken to ensure that raspberry plants that are propagated for commercial sale are virus-free, the perennial growth habit of the plant, which may be cultivated for ten years or more, means that it is exposed to virus diseases in the field for a considerable time allowing for a continual build up of infection. When this is combined with the modern approach of growing the plants under a protective tunnel, which increases both temperature and humidity around the plant, there is ample opportunity for new viruses or new combinations of viruses to move into the crop.

Under experimental conditions, a few raspberry viruses, e.g. *Raspberry bushy dwarf virus* and *Raspberry ring-spot virus*, can also infect herbaceous plants and this has made it possible fairly easily to isolate and characterise them. Many other viruses, e.g. *Raspberry leaf spot virus* (RLSV), *Black raspberry necrosis virus* (BRNV) and *Raspberry vein chlorosis virus* (RVCV) are restricted to raspberry plants and are present only at very low levels. This has made them very difficult to study and indeed until very recently all three were only characterised by the apparent symptoms they cause when



**Figure 1** Leaf symptoms of a plant infected with RGLBV and leaf and bud mite.

infecting particular raspberry varieties. Work done in the USA and at SCRI has now provided genome sequence information for BRNV and RLSV, allowing PCR-based diagnostic tests to be developed. The identity of RVCV still remains elusive.

To obtain further sequence information for raspberry viruses we have been analysing double-stranded (ds) RNA isolated from plants grown in plantations in Fife and Tayside that were showing symptoms of infection such as leaf curling and chlorosis. Production of dsRNA is a characteristic of virus infection, and it can be purified by binding to cellulose powder, allowing it to be concentrated and separated from plant-derived nucleic acids. The dsRNA is then reverse-transcribed into cDNA using random primers and either cloned directly or PCR amplified before cloning. Using this approach we have identified three new viruses, one of which we have completely sequenced.

One virus is most closely related to White clover cryptic virus 1, which is a member of the Alphacryptovirus genus and has a genome comprising two dsRNA molecules. An unusual feature of these viruses is that they are transmitted by infected ovule and pollen to the developing seed but otherwise have no cell-to-cell or systemic movement in the plant and are not graft transmitted.

The second virus has only two known relatives, Wheat mosaic virus and Pigeonpea sterility mosaic virus. These two viruses are rather difficult to work with and have not been characterised in much detail, however, they are thought to have multiple genome segments comprised of negative strand RNA. This means that the virus RNAs present inside the virus particle cannot be translated directly into viral proteins, and so an amount of viral polymerase protein must be included within the particle to initiate replication when the virus infects a new host plant. The wheat and pigeonpea viruses are



**Figure 2** Genome diagram of RuCMV.



transmitted by eriophyid mites, and we suspect that the raspberry virus, which we have named Raspberry green leaf blotch virus (RGLBV), is spread by leaf and bud mite, a pest that is of growing importance to the raspberry industry.

The third new virus, that we have named Rubus chlorotic mottle virus (RuCMV), is a member of the Sobemovirus genus. This virus has a small, positive-strand RNA genome that is encapsidated in spherical particles. We have obtained the complete sequence for this virus, showing that it encodes four major proteins:

ORF1, a pathogenicity protein; ORF2, a cysteine protease; ORF3, an RNA polymerase that is expressed by frameshifting as a C-terminal fusion to ORF2 protein; ORF4, the coat protein. We have constructed a cDNA clone of RuCMV from which we can produce synthetic RNA transcripts that are fully infectious when inoculated to herbaceous plants. This confirms that our derived sequence is authentic, and will allow us to do in-depth reverse-genetics studies to understand the molecular details of RuCMV biology.





# Plant Products and Food Quality

**Derek Stewart**

*The Plant Products and Food Quality programme, formerly called Quality, Health and Nutrition, conducts research into the chemical, biochemical and genetic bases of quality and bioactivity in plant-derived foods and products. It aims to enhance the health benefits of foods to the public by improving the nutritional and organoleptic properties of both raw and processed products and to establish diversification of the non-food crops sector via bioactive plant product research.*

Over the last year the programme has undergone a period of repositioning and reemphasis. Managed sustainability of renewable resources is now de rigueur in all aspects of agriculture and, along with a necessity to diversify the national (and UK) economy base, significant opportunities exist with respect to the development of plant products/non-food crops in the widest sense.

**Food Quality** The programme still retains a major focus on plant-derived food quality and the fundamental chemical, biochemical and genetic factors underpinning this. One of the quality targets is potato flavour. Building on our previous studies, we are investigating the biosynthesis of potato volatiles, an important component of potato flavour. However the soluble, matrix-associated

compounds also contribute to potato flavour and these have received less attention. Sensory taste scores gave a good correlation between high levels of umami compounds and positive aspects of potato flavour such as flavour intensity and overall acceptability. We aim to extend these observations to a wider range of germ-plasm and segregating populations. This approach is being extended significantly by further microarray work funded by the British Potato Council within which gene expression will be analysed and compared during tuber development and, importantly, also during the storage phase.

This core base of potato quality research has attracted significant external funding. Previous work on caro-



tenogenesis in potato tubers is being extended in an EU-funded integrated project (EU-SOL) to investigate the genetic basis of carotenoid formation amongst many quality traits. In addition the new EU-STREP DEVELONUTRI, coordinated by Dr Stewart, aims to develop and validate state-of-the-art metabolite profiling and analysis platforms that can be deployed at all stages in the crop improvement, production and processing platforms to ensure optimised quality, nutritional value and safety throughout the food chain. The project's focus crops will be potato, wheat and tomato.

Potato biodiversity and development are intimately linked with the programmes food quality research. Indeed a comparative metabolomic study of cultivars and landraces has shown considerable variation in mainly the many polar metabolites that could be exploited to manipulate quality traits. This will be further supported by a Royal Society Joint Project grant with Professor Uwe Sonnewald, University of Erlangen, Germany, to exploit the potato microarray and elucidate the mechanisms of tuber dormancy release and sprouting.

The more translational aspects of post harvest quality are being addressed via Scottish Enterprise Proof of Concept Funding to develop and exploit additive-free methods for extending the shelf-life of minimally processed foods (e.g. prepared salads).

Food quality research also extended to soft fruit with the completion of a five year horticulture LINK programme to examine vitamin C accumulation in blackcurrant. The work represents the first time that vitamin C accumulation in sink tissues (e.g. fruits, tubers) has been systematically examined on a whole-plant system level taking into account both synthesis in the sink tissue and transport from photosynthetic tissues or storage pools. Predictive molecular markers for fruit vitamin C content were identified. Incorporation of these markers into the SCRI blackcurrant breeding programme should significantly reduce the time to release of new cultivars.

**Food Safety** Food safety is either directly or indirectly at the heart of all food matters and genetic modification is the focus of several plant-food safety projects with two funded by the Food Standards Agency to develop a practical method for reliably determining transgene junc-

tion sequences and a metabolomics-based approach to develop unified strategies for handling processing and analysing metabolomics data with a view to using these approaches to assess GM crop safety. At the EU level, the recently completed project NOFORISK ([www.noforisk.org](http://www.noforisk.org)) showed via *in vitro* and *in vivo* physiological, transcriptomic and metabolomics studies that for the selected GM potato under study, their exposure (including consumption) to mammalian systems was accompanied by no significant deleterious effects.

SCRI co-ordinates a major work package in the EU FP6 project SAFEFOODS ([www.safefoods.nl](http://www.safefoods.nl)) which addresses the issue of how consumer confidence in consumer protection and risk analysis can be restored and strengthened. The work package is assessing some of the key drivers of variation in gene, protein and metabolite expression in potato tubers and maize kernels using “omics” approaches. This benchmarking of variation, taken together with the concept of history of safe use, can be used to place into context any “unintended” variation revealed, for example in genetically modified crops. From an extensive analysis of field grown crops the project is demonstrating that genotype, site and season differences are major drivers of variation, but it has proven extremely difficult to distinguish GM crops from their non-GM controls in the cases studied. However, over three growing seasons it has been possible to distinguish between organic and conventionally grown crops of potato using “omics” approaches (collaboration with Prof C. Leifert, University of Newcastle). Data are now emerging on some of the genes, proteins and metabolites driving such differences.

**Plant Products and Bioactivity** Bioactives research within the programme has exhibited a broad brush. A study has been undertaken into the relative concentration, distribution and utility of calystegines (Figure 1), potential pharma feedstock compounds, in potatoes. Collaborations with biomedical researchers have shown that ellagitannins in raspberries exhibit anti-cancer activity *in vitro* and this is being addressed in depth via joint PhD studentships with the University of Ulster and Dundee to study the effects of fruit components on genotoxicity, apoptosis and invasiveness in colon cancer cells and cancerogenesis *per se*, respectively.

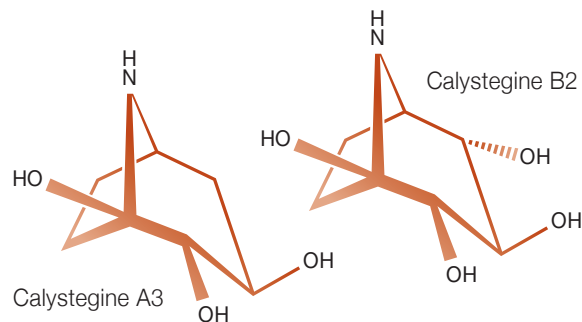


Figure 1 The main calystegines found in potato.

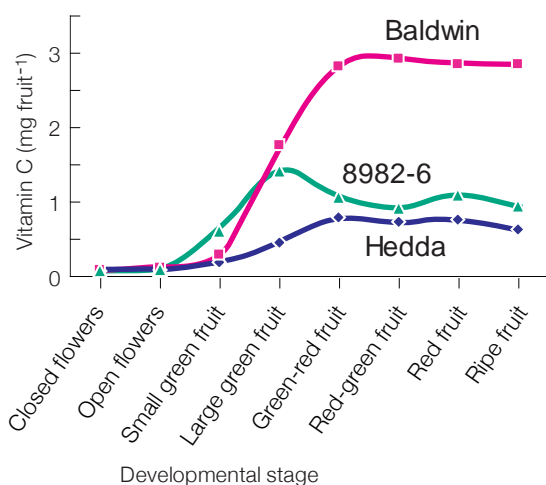
Finally, food functionality and bioactivity is the focus of Barleybread, an EU project aiming to use barley as a functional diluent for wheat in bread. The project aims to exploit functional diversity in barley, such as  $\beta$ -glucans, antioxidants etc., and to identify lines elevated in these components with a view to their inclusion in bread-making and to assess how this inclusion impacts upon taste, texture and nutritive value.



# Mechanism of vitamin C accumulation in blackcurrant fruit

Paul G. Walker, Simon D.A. Pont, Nicola Marquis & Robert D. Hancock

In recent years, there has been intense interest in the biosynthesis, metabolism and physiological functions of vitamin C in plants. Considerable advances have been made in understanding the biosynthesis of vitamin C with the publication of the *de novo* pathway in 1998 and the subsequent identification of three alternative pathways. In addition, breakthroughs have been achieved in understanding vitamin C catabolism with the identification of enzymes and pathway intermediates involved in the synthesis of oxalic, threonic and tartaric acids from vitamin C. Finally, significant strides have been made in understanding the role of vitamin C in various aspects of plant physiology and it has become clear that the vitamin plays an essential role in the modulation of reactive oxygen signalling which has implications for a range of plant responses to developmental, biotic and abiotic stimuli.



**Figure 1** Numbers of nematodes developing on plants after exposure to double-stranded RNA targeting chorismate mutase (red bars) or a control gene (GFP – blue bars).

Despite these advances, very little attention has been paid to how vitamin C accumulates in the plant sink tissues (fruit, tubers) that form a major part of the human diet. Work undertaken at SCRI and elsewhere has shown that vitamin C synthesis can occur in heterotrophic (non-photosynthetic) tissues, however, it is also known that vitamin C can be transported from actively photosynthesising leaves to fruits and tubers (Tedone *et al.*, 2004). Uncertainty remains regarding the contribution of each source towards the accumulation of vitamin C in heterotrophic plant tissues.

Blackcurrants are exceptionally high in vitamin C with typical commercial cultivars containing 160 mg per 100 ml juice, approximately four times the amount found in orange juice. Historically, they were highly prized for their high vitamin C content and this trait remains an important target in modern breeding programmes. In order to help define molecular targets for accelerated breeding, a systematic analysis of the mechanism of vitamin C accumulation in blackcurrant fruit was undertaken (Hancock *et al.*, 2007). This is the first time that such an analysis has been performed for any crop.

Vitamin C accumulated early in fruit development during the expansion stage and prior to the development of red, blue or black colouration (Figure 1). In order to test the vitamin C transport hypothesis, radiolabelled vitamin C was supplied to leaves and translocation to fruit determined. Only 1% of the supplied radioactivity was recovered in fruit after 48h suggesting that transport was not an important mechanism for vitamin C accumulation in fruit. Furthermore, at the time of maximum fruit vitamin C accumulation leaf biosynthetic capacity halved contrary to what would be expected if leaves were supplying significant amounts of the vitamin to fruit.

In fruit, rates of both vitamin C biosynthesis and degradation varied with fruit maturity. In young fruit that were actively accumulating vitamin C, biosynthesis was high and degradation low and this situation was reversed in older fruit where vitamin C accumulation had ceased.

Taken together, these data support the contention that in blackcurrant fruit vitamin C accumulation occurs as a result of *in situ* biosynthesis and that transport from





distant organs does not provide a major contribution to fruit vitamin C levels. Instead, sugars are synthesised in leaves and transported to fruit providing the substrate for vitamin C synthesis. These findings allow the search for predictive markers of fruit vitamin C levels to be focused on biosynthetic genes and specific variations within one of the biosynthetic genes has already been associated with high vitamin C content. By testing for these genetic variants at the seedling stage, rather than waiting four years for plants to mature, selections can be made at a much earlier stage. This will result in the accelerated breeding of high vitamin C cultivars. Such an approach could be transferred to other fruits and vegetables that have a long generation time.

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#### Acknowledgments

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# Environment Plant Interactions

**Philip J. White**

*The EPI Programme comprises three Teams. The Resource Capture Team seeks to optimise energy, mineral and water use by crops for sustainable economic and environmental benefits. The Plant–Soil Interactions Team investigates the belowground interactions between plants and their abiotic and biotic environment, applying knowledge from a wide range of disciplines to monitor, understand and advise on soil resilience, sustainability and environmental quality. The Agroecology Team scales between individual interactions and landscape processes, to anticipate responses to agricultural innovations and global change. Together, these teams combine to translate basic scientific research into solutions for current and future challenges for agroecosystem management in a changing world.*

The [Resource Capture Team](#) is addressing the need to maintain crop yields whilst reducing fertilizer inputs and irrigation. Philip White has already identified genetic loci affecting mineral acquisition, yield with reduced fertilizer inputs, and tissue mineral concentrations in brassica crops in collaboration with researchers at Warwick HRI and Nottingham University. This knowledge can be used to develop genetic markers for breeding programs. In collaboration with the Genetics Programme, this Team

are screening the extensive barley and potato collections available at SCRI for superior genotypes in both glasshouse and field experiments. This research effort has been strengthened by the appointment of two Research Leaders: Tim George, who is studying how resource acquisition can be improved through manipulation of the rhizosphere, and Lionel Dupuy, who is modelling how plant genotype affects root architecture and resource acquisition. The recent purchase of



an inductively coupled plasma mass spectrometer has enabled a wide range of elements to be assayed, which not only facilitates work on the mineral nutrition of plants but also our investigations of the role of plant chemistry in plant-insect interactions and the effects of agriculture on geochemical processes.

[Alternatives to conventional inorganic fertilisers](#) are being trialled at SCRI. These include the phosphorus-rich product 'struvite', which can be reclaimed from sewage, and nitrogen-rich composted municipal waste. This year, Ron Wheatley undertook agricultural trials sponsored by the UK's Waste & Resources Action Programme (WRAP) to investigate the market opportunity for quality green composts in both conventional and organic systems producing barley and potatoes. In these trials, effects on weeds and disease incidence, and soil health, moisture retention and permeability and soil carbon levels, are being assessed in addition to crop yield and quality. Previous field trials with spring barley showed enhanced crop establishment and development during the early growth stages and a significant increase in grain yield.

[The Plant-Soil Interactions Team](#) has been investigating how roots grow through the soil and how this knowledge can be used to ameliorate adverse soil conditions for crop production. Glyn Bengough and colleagues from the Norwegian University of Life Sciences have been tracking the local deformations and changes in substrate density around roots as they grow through soil. Using maize mutants, they have demonstrated the importance of the root cap in this process. In parallel, computer-vision techniques for quantifying root growth and development are being developed by Nathalie Wuyts, Tracy Valentine and Lionel Dupuy in collaboration with scientists at the Universities of Cambridge, Dundee and Abertay. In work supported by the Mylnefield Trust, Blair McKenzie is developing field and glasshouse assays to identify barley varieties better able to penetrate compacted soils and exploit limited water availability.

[Physical stresses experienced by field crops during the growing season](#), have also been investigated by this Team. These appear to depend on the location

of plant roots in the soil profile. During the dry spring of 2007, they observed that the barley crop experienced mechanical impedance as the dominant physical stress, followed by periods of hypoxia in the very wet summer months before harvest. In addition, using techniques developed by Paul Hallett in collaboration with scientists from the University of Kiel, they observed that compaction stresses from tractors caused irreparable damage to the subsoil under these environmental conditions. A major EPSRC research project on ecoengineering of slopes with vegetation was also completed. This project, led by Glyn Bengough and Paul Hallett in collaboration with the Geotechnical Engineering Group at the University of Dundee, combined knowledge of soil mechanics and plant sciences to understand how plant roots reinforce soil and prevents slopes collapsing.

[The EU ECOGEN Project](#) was successfully completed this year and eleven papers from this project were published in a Special Issue of *Pedobiologia* edited by Bryan Griffiths (SCRI) and Paul Henning Krogh (University of Aarhus). This project brought together eight academic partners from five EU countries plus Monsanto to investigate the ecological and economic consequences of introducing GM crops to agriculture. It concluded that transgenic maize expressing either herbicide resistance or an insecticidal protein from *Bacillus thuringiensis* had no deleterious effect on soil biota, demonstrated the effectiveness of *Bt*-maize against the European Corn Borer, generated a predictive model to summarise the effects of soil organisms on soil quality, and suggested that, while the immediate economic benefits from adopting *Bt*-maize were small, the benefits foregone from non-adoption could be several million Euros per year for the EU-15.

[The Agroecology team](#) successfully completed the EU SIGMEA Project. This project studied gene flow in the environment, which determines whether coexistence is feasible between different forms of crop production. Geoff Squire coordinated the collation of experimental results from 24 scientific partners throughout Europe to produce the most comprehensive synthesis available of experimental data on cross pollination, seed persistence and movement, and ecological impacts in relation to the introduction of GM crops. This data has enabled the





Soil sampling for biodiversity across arable fields in the East of Scotland.

development of novel conceptual models for scaling from the individual to the landscape and produced unique insights on commonalities and differences in gene flow in the environment between geographical regions. This knowledge has linked the science of gene flow with policy on biodiversity and genotypic coexistence within the EU and its member states.

[A survey of arable biodiversity and resilience](#) in the east of Scotland, covering 60 farms from mid-Lothian to Moray, has been initiated by Cathy Hawes. This survey, together with a collaborative BBSRC-Link project with Rothamsted Research, is extending the datasets obtained during the Defra Farm Scale Evaluations to provide data for modelling the influence of trophic interactions on farmland species diversity and the ecological consequences of changes in agricultural management. This work is also providing an opportunity to discuss our research directly with farmers and assess their attitudes towards arable management, biodiversity and sustainability. In tandem with these field studies, Jane Wishart and Pete Iannetta are

developing genetic markers for plant functional-traits, to enable intra-specific diversity of weed populations to be monitored and predictions of biodiversity and ecosystem services to be made.

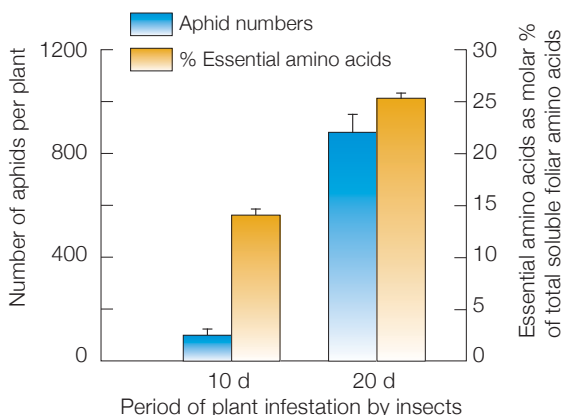
[Assays of community structure using genotyping techniques](#) have also been developed for commercial applications. EnPrint™ is an emergent spin-out company being incubated within EPI under the auspices of Mylnefield Research Services. Using state-of-the-art molecular genotyping techniques developed through Proof of Concept Awards, Tim Daniell and colleagues aim to overcome the limitations of traditional taxonomic methods for obtaining biological indices of environmental quality. To demonstrate the efficacy of this approach they have developed a marine-monitoring assay, based on quantifying the abundance of different pelagic algae, in collaboration with the Scottish Environment Protection Agency (SEPA). They are now in the process of beta-testing a commercial system in the marketplace before offering a full commercial service in 2008.



# Aboveground– belowground trophic linkages

**Scott N. Johnson, Alison J. Karley, Cathy Hawes & Carolyn Mitchell**

Plants are attacked by an array of pests and pathogens at the same time, so little wonder that many of these organisms affect each other by inducing physiological changes in their shared host plant. Plant and insect physiologists now recognise that these interactions could have important consequences for sustainable pest management in crop production. For example, simply targeting one pest could inadvertently lead to unanticipated surges in others. This is likely to be particularly true for pests that target different parts of the same plant, and root-feeding and foliar-feeding insect pests are known to affect each other through plant-mediated mechanisms even though these insects never physically meet (Wardle *et al.*, 2004). Root-feeding insects are frequently overlooked because they live in the soil and are less visible, so large populations can develop before growers spot the problem. We have begun to characterise the linkages between aboveground and belowground insect pests in several systems, ranging from barley to red raspberry, focusing on the changes in plant chemistry which underpin these interactions.

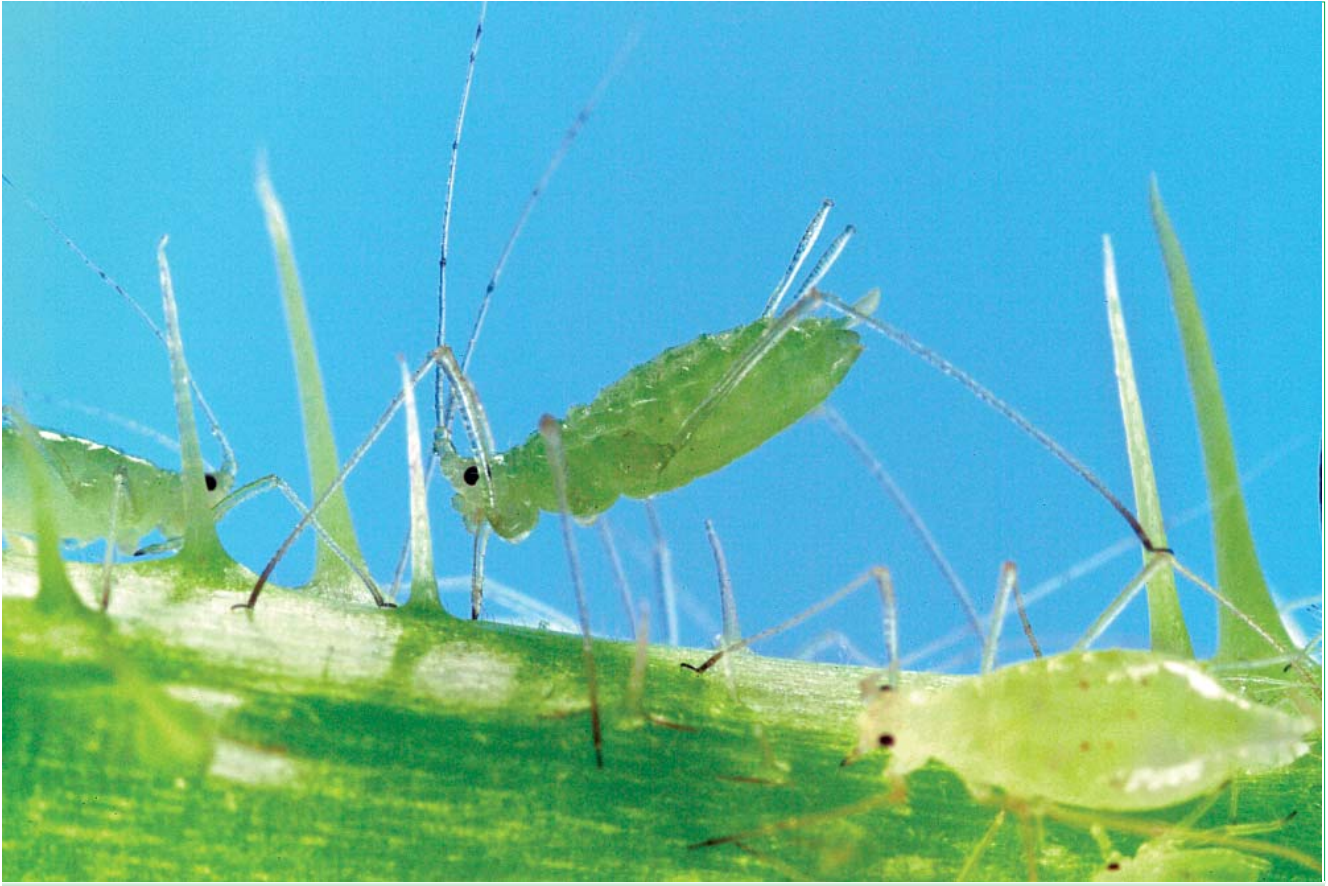


**Figure 1** Impacts of root-feeding wireworms on aboveground populations of *R. padi* and foliar amino acids.



Our most recent research has explored the interactions between root-feeding wireworms (not worms at all, but juvenile stages of the *Agriotes* spp. click beetle) and the foliar-feeding bird cherry oat aphid (*Rhopalosiphum padi*) on barley. These aphids are known to transmit several viruses to barley which can severely reduce crop yields. Wireworms, in contrast, are a relatively new pest of cereals (conventionally a problem in potatoes; Johnson *et al.*, 2008) which have begun to affect many Scottish growers due to changes in management practices (e.g. declining residues of soil pesticides and increased irrigation). Our latest findings suggest that if barley plants are simultaneously attacked by both insects during certain stages in plant development, root-herbivory by wireworms can lead to increases in *R. padi* populations of more than 30% (Figure 1). Greater numbers of aphids in the presence of wireworms might be due to wireworm-induced changes in foliar amino acid composition, which reflects the food resource available to aphids, as aphid numbers correlated with the proportion of leaf essential amino acids (Figure 1). Moreover, simultaneous attack by both insects causes changes in important plant mineral nutrients such as phosphorus, sulphur and calcium. We aim to address how these changes affect plant health and the performance of insect pests.





In red raspberry we have discovered that even moderate root-herbivory by the vine weevil (*Otiorhynchus sulcatus*) compromises genetically inbuilt aphid resistance in some cultivars. For instance, when two vine weevils fed on the roots of Glen Clova plants, populations of the large raspberry aphid (*Amphorophora idaei*) increased by 80%. This is significant because the large raspberry aphid transmits at least four raspberry viruses and remains the most damaging aphid pest of commercial raspberry production in the UK.



It is clear from this research that aboveground–belowground trophic linkages could have important implications for how breeders and growers address pest control in the future. With greater understanding of the chemical and genetic mechanisms underpinning such aboveground–belowground interactions, it may become possible to control such interacting pests much more effectively in the future.

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# Phosphorus Efficient Potatoes

**Tim George, Lawrie Brown, Jane Wishart,  
Jacqueline Thompson, Gladys Wright, Gavin  
Ramsay, John Bradshaw, Philip White**

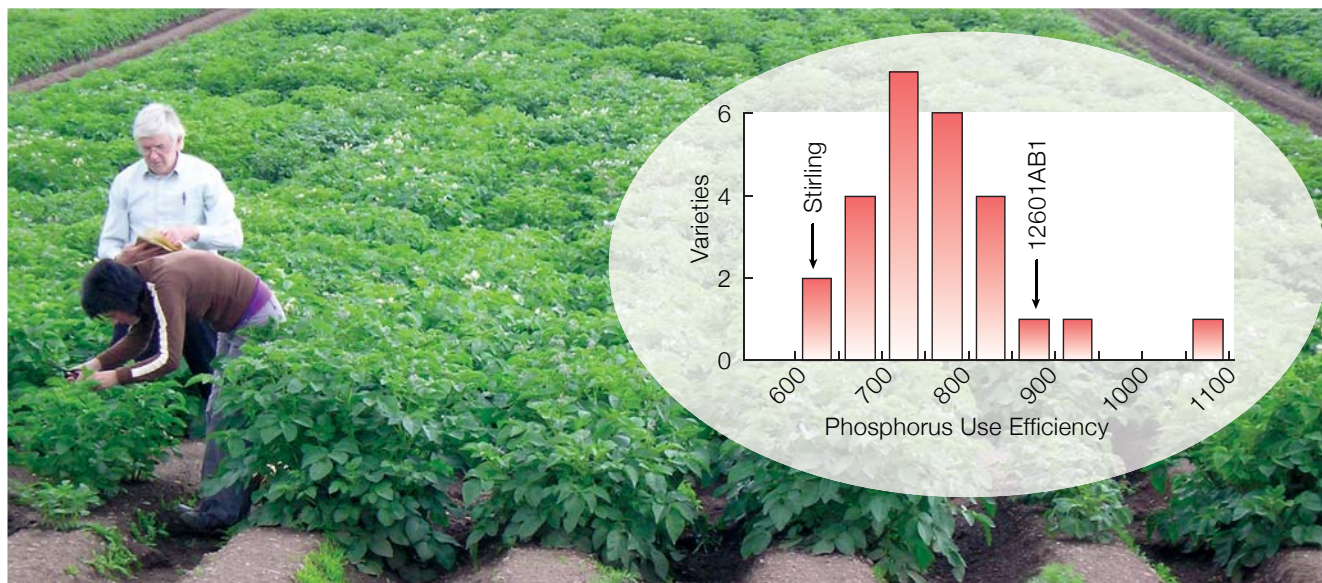
Phosphorus (P) is a mineral nutrient required by plants and its management in soil is critical to ensure a sustainable and profitable agriculture that has minimal impact on the environment. Although soils contain large amounts of P, only a small proportion is immediately available to plants. For this reason, P-fertilisers are commonly used to maintain agricultural productivity. However, intensive use of P-fertilisers has resulted in the accumulation of P in soils, albeit in forms that are poorly available to plants. The movement of this P to water-courses is of environmental concern. Our objective is to improve the economic and environmental sustainability of agriculture by using fertilisers more efficiently.

Potatoes require large P-fertiliser inputs. One way to reduce these inputs is to cultivate genotypes that use P efficiently, either because they require less P in their

tissues or because they yield with smaller P input. These abilities are affected by many factors, but rooting characteristics (such as increased rate of growth, specific root length, and density and length of root hairs) and rhizosphere biochemical processes (such as the exudation of organic acids and enzymes) are of fundamental importance. Understanding the physiological and genetic control of changes in these characteristics as a natural response to P deficiency may provide opportunities to improve the acquisition of soil and fertiliser P by plants in conventional and organic systems.

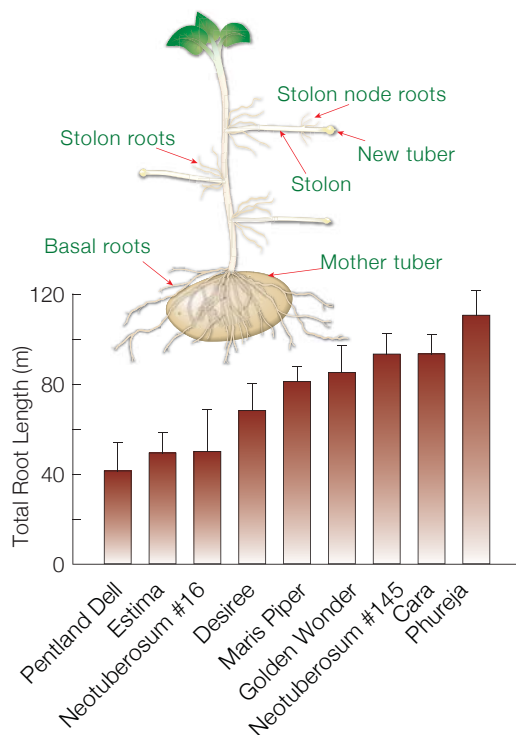
Our initial approach has been to screen core collections for tissue P efficiency (PUET) in tuber yield (Figure 1). This work has demonstrated significant differences in PUET between commercial varieties and, importantly, between parents of SCRI genetic mapping populations. In a Defra-funded collaboration with Dr John Hammond (Warwick HRI) we have screened these populations for PUET and identified chromosomal regions (QTL) affecting this trait.

We have also assessed the ability of potatoes to explore the soil volume, by screening genotypes for rooting characteristics in the field (Figure 2). We found significant differences in root length between commercial



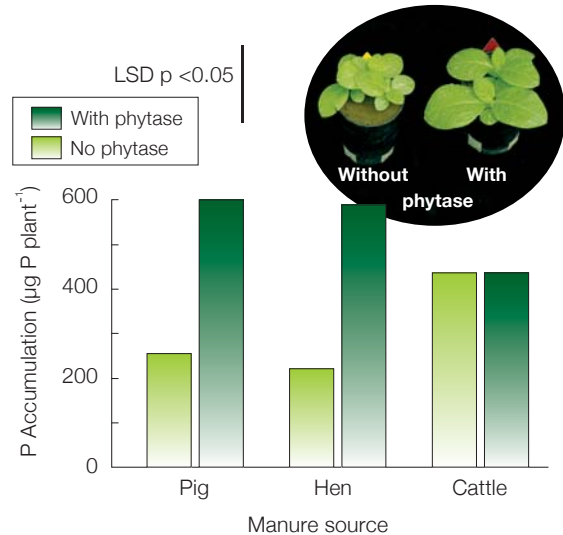
**Figure 1** Screening genetic mapping populations of potatoes for P-use efficiency in the field is identifying the genetic basis of traits that will deliver varieties that allow sustainable reduced-input agricultural production. Inset: Phosphorus Use Efficiency (g DM / g P) determined in tubers of a core collection of 26 commercial potato varieties trialled in the field at SCRI in 2006. Data are means of two replicate plots each containing eight plants at 40 cm spacing. Stirling and 12601AB1 are parents of a *Solanum tuberosum* genetic mapping population.





**Figure 2** Total root length (m) of field grown potato plants excavated at tuberisation in the 2007 growing season. Potato varieties screened included European tetraploid potato (*Solanum tuberosum* Group *Tuberosum*), a diploid Phureja potato (*Solanum tuberosum* Group *Phureja*) and some neotuberosum germplasm. Plants were grown at an 80 cm spacing. Data are the means of four replicates with standard error presented as a bar. Inset: Representation of potato rooting system.

varieties. In future research, this trait might be exploited in breeding programs for improved P acquisition. In addition, we are studying the ability of plants to mobilise sparingly-soluble soil P. In collaboration with Dr Alan Richardson (CSIRO, Australia) we have expressed extracellular phytase genes in plants, in an attempt to improve P acquisition from organic compounds in the soil. Recent experiments compared plants grown in soils that had been amended with manures from monogastric animals, which is thought to contain high concentrations of phytate (the substrate of phytase), with those grown in soils amended with low-phytate



**Figure 3** Accumulation of P by plants expressing extracellular phytase genes compared to controls without phytase, when grown in soils amended with manure from monogastric animals (Pig, Hen) and that from ruminants (Cattle). Data are the mean of five replicates and LSD ( $p < 0.05$ ) is shown as a bar. Inset: Growth of tobacco plants with and without the expression of phytase.

manure from ruminants (Figure 3). Plants expressing extracellular phytases had greater P-uptake than untransformed controls when grown in soils amended with high-phytate manures, but had no advantage in soils amended with low-phytate manures. These results suggest that it may be possible to enhance P-acquisition by potatoes by increasing rhizosphere phytase activity. This might be achieved by expressing phytase genes in commercial germplasm or by fostering phytase exuding microorganisms in the rhizosphere.

The research being performed by the EPI Resource Capture Group is enhancing our physiological understanding of traits affecting potato P nutrition and their genetic control. This will allow us to select potato varieties requiring less fertiliser P, fulfilling our objective of reducing P-fertiliser inputs to potatoes, thereby increasing the economic and environmental sustainability of this enterprise.



# Division of Plant Sciences University of Dundee

**John W. S. Brown**

*The Plant Sciences Division conducts basic research into how plants grow and develop in response to their environment, biochemical processes and biotechnological developments, and genome structure and plant biodiversity. The University of Dundee plant scientists have been located on the SCRI campus since 2003. In 2007, the College of Life Sciences created the Division of Plant Sciences presenting a major opportunity for UoD plant scientists to establish a strong identity both within the College and internationally and to build and expand on the partnership between SCRI and CLS.*



The new Division of Plant Sciences is made up of eight research groups: the original five University groups at SCRI (Andy Flavell, Claire Halpin, Lyn Jones, John Raven and Gordon Simpson) along with Steve Hubbard, who has recently re-located from the University campus, and the appointment of Paul Birch and John Brown to personal chairs. Prof. Carol MacKintosh of the MRC Protein Phosphorylation Unit is an affiliate member of the Division due to her interests in control of plant

metabolism by phosphorylation and 14-3-3 proteins. John Brown heads the Division with Claire Halpin as Deputy Head, who also received a well-deserved personal chair in 2007.

The goals of the Division are to increase its international standing in basic plant sciences, to bring in significant external funding and publish in the best journals, and to attract excellent plant scientists to a career in Dundee. It



will also expand the already successful interactions with SCRI scientists and research groups which have led to substantial joint funding and new opportunities.

The main activities of the Division's research groups in 2007 are summarised below:

**Transposons, genome evolution and biodiversity (Dr Andy Flavell)** Dr Andy Flavell's research is centred upon genome structure and evolution in crop plants. Crop genomes have been selected from wild ancestors by thousands of years of human selection, leading to a big reduction in biodiversity. The Flavell group has developed and used molecular markers to study this diversity. These markers are being applied to the improvement of fungal resistance in wheat and potato by breeding, in partnership with SCRI (Robbie Waugh, Glenn Bryan) with the support of the European Commission (EU Framework 6 project BIOEXPLOIT; joint value to SCRI/UoD £1.25 million; <http://www.bioexploit.net/>). The Flavell group is also involved in another EU-sponsored project analyzing field pea biodiversity (Project GRAIN LEGUMES). The lab collaborates closely with Dr David Marshall and colleagues at SCRI to refine the GERMINATE database for storing, manipulating and displaying data related to plant biodiversity. This work is supported by both BIOEXPLOIT and a UK BBSRC Project grant (GERMINATE 2; <http://bioinf.scri.ac.uk/germinate/wordpress/>) which began in 2007. Finally, the Flavell group is coordinating a consortium that includes SCRI (Joanne Russell, Robbie Waugh) and five mainland European cereal genomics labs with the goal of developing a novel association mapping approach for capturing useful new gene alleles from wild and landrace barley and transferring them into cultivated germplasm, funded by ERA-PG Programme (<http://www.erapg.org/>).

**How plant pathogens trigger, suppress or manipulate host defences (Prof. Paul Birch)** To suppress or otherwise manipulate plant defences, pathogens secrete molecules that can interact with host cells. In some cases these virulence determinants (effectors) are delivered (translocated) inside plant cells where they directly interact with host proteins, re-programming host defences to the pathogen's benefit. Prof. Birch's

group focuses on two economically important pathogens of potato, the oomycete *Phytophthora infestans*, which causes late blight disease, and the enterobacterium *Pectobacterium atrosepticum*, which causes blackleg and soft rot. A major goal is to understand the key plant defence pathways that must be manipulated in order to establish a susceptible environment for disease development. The group is funded to study *P. infestans* effector functions via EU BIOEXPLOIT and the BBSRC Crop Science Initiative (in collaboration with Drs Steve Whisson and Leighton Pritchard at SCRI). A RERAD-funded systems biology project and BBSRC-RERAD jointly funded project (in collaboration with Drs Ian Toth and Leighton Pritchard at SCRI) seek to identify and characterize the major virulence determinants in *Pectobacterium*, and to understand the central components of plant defence that are targeted by this pathogen.

**Manipulation of plant metabolism using reverse genetics (Prof. Claire Halpin)** Understanding and manipulating the composition and structure of plant cell walls has become a major research objective worldwide due to the current interest in producing bioenergy and biofuels from plant biomass. There have been many new funding opportunities in this area in 2007 that we have been quick to exploit, leading to several new projects in the Halpin labs. Dr Jennifer Stephens is embarking on a BBSRC-funded project on the molecular-genetics of lignin biosynthesis in barley, in collaboration with Robbie Waugh and several of his team in the Genetics Programme. This work will include TILLING for lignin mutants in barley. Man-power on the project is supplemented by a BBSRC Targeted Priority Studentship in Crop Science awarded to Paul Daly. A Collaborative Research proposal to the FP7 call on Plant Cell Walls has also been successful and the €6 million project, coordinated by Prof. Simon McQueen Mason (York University), will start early in 2008. The Dundee role in this project is to investigate lignin biosynthesis in the emerging monocot model species, *Brachypodium*. This new work will have significant synergies with the on-going barley work. A programme grant, jointly held with Dr. Gordon Simpson, from the GCEP (Global Change and Energy Project) at Stanford University will





shortly allow us to begin more basic gene-discovery work on cell wall biosynthesis in *Arabidopsis*. Work continues in the area of plant recombination and gene targeting under a Leverhulme grant that funds Dr. Abdellah Barakate. This work is also leading to increasing collaboration with the Genetics programme, principally with Dr Luke Ramsey, with whom we have a BBSRC LOLA application in the process of evaluation.

**RNA processing and expression (Prof. John W. S. Brown)** Plant growth and development, and how plants respond to pathogens and the environment in which they grow, reflect complex gene expression patterns. The Brown lab is interested in how gene expression in plants is modulated by post-transcriptional processes such as alternative splicing and small non-coding RNAs. The importance of alternative splicing is well recognised in animals due to many diseases being caused by mutations affecting splicing and alternative splicing. In plants, around 35% of *Arabidopsis*/rice genes are estimated to undergo alternative splicing. Key questions are 1) which plant factors determine splice site selection,

2) how do particular combinations of factors in different cells and tissues determine tissue-specific alternative splicing, and 3) how are alternative splicing patterns and levels of splicing factors affected by environmental and developmental cues? John Brown and Craig Simpson (SCRI) have established an accurate and reproducible RT-PCR system to examine 400 alternative splicing events simultaneously. This provides the basis for studying the effects of RNA-interacting proteins involved in aspects of mRNA biogenesis on splicing and alternative splicing. This particular research area receives funding from the European Alternative Splicing Network of Excellence (EURASNET) in collaboration with the labs of Andrea Barta and Artur Jarmolowski in Vienna and Poznań.

**Regulated gene expression controlling flowering (Dr Gordon Simpson)** Gordon Simpson's lab is studying how plants regulate gene expression to control the time at which they flower. Gordon's lab has been studying an RNA binding protein called FPA that promotes flowering. In order to understand how it does this, the key



question they are trying to answer is: What RNAs does this protein bind? With funding from the BBSRC, Lionel Terzi, working in Gordon's lab, has successfully developed methodology to "fix" the interactions of an RNA binding protein to its target RNAs inside living cells. He has now used this methodology with FPA, so we should soon learn what the target RNAs are. To identify the RNAs, The Simpson lab is using state-of-the-art Solexa sequencing technology to sequence all the RNAs in *fpa* mutants. Katarzyna Rataj joined the lab in 2007 as a PhD student, funded by the BBSRC, and is focusing on identifying the proteins that FPA interacts with. This combination of approaches should tell us not only how FPA functions in controlling flowering, but provide a generally applicable strategy to uncover the function of the many RNA binding proteins that are specific to plants.

[The dynamics of plant-aphid-microbe associations \(Dr Steve Hubbard\)](#) The Hubbard group is concerned with the population dynamics of insect-microbe associations and the factors which affect these interactions. A considerable proportion of our work has been centred on the development of novel modelling techniques with which to describe these dynamics, and we have published several papers in recent years which describe the application of these ideas to host-parasitoid-bacterial associations. The principal experimental models for testing such techniques are insect parasitoid-host systems, and the endosymbiotic bacteria which are often associated with one or both partners. Dr Hubbard's move to SCRI has opened up a number of opportunities to develop this research in the context of aphid-parasitoid interactions, because aphids are host to a considerable community of primary and secondary bacterial endosymbionts, which have the capacity to influence the fitness of the aphid host and consequently its capacity to vector plant pathogens. He is also interested in the way in which these fine-grained phenomena affect broader scale issues such as community dynamics and biodiversity amongst insects in farmland habitats.

[Plant ecophysiology and adaptation to environmental stress \(Prof. Hamlyn Jones\)](#) Research in Prof. Lyn

Jones's group aims to understand the ways in which plants can tolerate individual environmental stresses such as drought and salinity as a basis for improving both the genotypes available for agriculture and for improving crop management for stressful conditions. A key development has been the use of thermal remote sensing for detecting water stress in crops and this year the group has successfully applied this technology to the phenotyping of rice cultivars for drought tolerance in collaboration with groups in the Philippines, Huazhong Agricultural University and the University of Aberdeen. In related work the group is also developing thermal sensing as a tool for the automated scheduling of irrigation in the Hardy Nursery Stock nurseries, while a larger-scale application for scheduling irrigation in vineyards has been tested in a large commercial vineyard in South Australia (in collaboration with CSIRO, Australia). A repeat trial is underway to confirm the reliability of the technique. In a new line of work the group is investigating the physiological mechanisms underlying the tolerance of some plants to soils containing high concentrations of heavy metals, particularly those on "serpentine" rocks. This is in collaboration with a group from the Bulgarian Academy of Sciences.

[Interactions among resources in the growth of phytoplankton \(Prof. John Raven, FRS\)](#) Diatoms deciphered: diatoms in the surface ocean account for up to a fifth of global primary productivity, yet many fundamental aspects of their functioning remain unclear. An example is the unexpected findings obtained with colleagues in Sheffield on the means by which carbon from dissolved carbon dioxide becomes organic carbon where two closely related species of marine diatom have different biochemical pathways of inorganic carbon assimilation. Work on another species of diatom with a German colleague led to the discovery of the first example of spontaneous oscillations in the rate of photosynthesis in a unicellular organism. While the mechanism of these oscillations is not yet fully understood, the results clearly show that some earlier interpretations of related phenomena in land plant leaves involving cell-cell interactions are not of universal applicability.







# Biomathematics and Statistics Scotland

**David A. Elston**

*Biomathematics & Statistics Scotland (BioSS) is a specialist organisation delivering high-quality consultancy, training and research in statistics, mathematical modelling and bioinformatics. BioSS forms a distinctive element of SCRI Group and plays a unique role in the Scottish research community, bridging the gap between research in the mathematically-based and traditionally more qualitative sciences such as biology.*

Many facets of the BioSS's scientific work are encapsulated in the new BioSS Vision statement:

*“ to improve science & society through an understanding of variation, uncertainty and risk.”*

We enhance understanding through process modelling and data analysis, as well as through the design of experiments and observational studies. Variation can be of a deterministic nature, or partitioned into uncontrolled components that we often think of as being random.

Uncertainty refers to our state of knowledge, which is always clouded by both measurement error and natural variation. At a probabilistic level, risk refers to the integration of variation and uncertainty, with attention often focusing on the chance of extreme events. Much of our work is directed towards scientific objectives, but with a widening range of outcomes including providing an

evidence base for improved policy making and contributing to economic activity through the levy boards and private sector organisations.

BioSS manages its consultancy work under the four broad scientific areas:

- *plant science;*
- *animal health and welfare;*
- *ecology and environmental science;*
- *human health and nutrition.*

In each area, BioSS staff have a wide range of different types of interaction with scientists, ranging from the provision of short pieces of advice that allow BioSS expertise to guide a large number of scientific research projects, through to deep collaborative relationships that allow BioSS staff to make substantial inputs to a small number of scientific projects in which quantitative



issues play a central role. Whilst the following highlights describe collaborative interactions, the cumulative importance of the advisory inputs should not be underestimated.

Our consultancy work for *plant science* supports scientists investigating the genetics of important Scottish crops such as potatoes, barley and soft fruit, the diseases that inhibit production of these crops, environment-plant interactions and the quality of plant-derived foods and other plant products. BioSS has recently developed a user-friendly program, TOPALi, to allow faster, more sophisticated statistical analyses of the evolutionary relationships among molecular sequences. This software includes novel recombination detection methods developed by BioSS and implements modern Bayesian methods of inference for phylogenetic analysis. It is currently being used to study microbial soil diversity, nematode taxonomy and relationships among members of multi-gene families.

Our consultancy work for *animal health and welfare* supports scientists investigating the bacterial, viral and parasitic diseases of farm animals, husbandry-related welfare issues and the interaction of agricultural practices in animal farming systems. BioSS has recently collaborated with the Scottish Agricultural College in the design and analysis of a survey of the prevalence of verocytotoxic *Escherichia coli* in the faeces and digestive tract of sheep sent for slaughter at Scottish abattoirs. This work has built on 10 years of collaboration with SAC veterinary epidemiologists in exploring the dynamics of this zoonotic infection in Scottish livestock, and has drawn on research carried out in BioSS in the statistical properties of zero-inflated models of infection prevalence in the presence of random effects. The results will be used by the Food Standards Agency in Scotland to inform future policy decisions relating to meat microbiological safety.

Our consultancy work for *ecology and environmental science* supports scientists investigating soil health, water quality, and ecological communities, with the aim of understanding and managing the interactions between the rural economy and the environment. In collaboration with The Macaulay Institute, we have

begun studying daily flow data for the River Dee dating back to 1929 to look for long-term changes in the distribution of flows, including changes in seasonal patterns and the size and frequency of unusual events. BioSS staff are employing their skills in time series analysis and modelling of extremes, in terms of both high flows (causing flooding) and low flows (when the highest concentrations of chemicals occur).

Our consultancy work for *human health and nutrition* supports scientists investigating chronic dietary-relations conditions such as obesity, cardiovascular health and gut health. Microarray studies have become a core part of this research. BioSS has collaborated with normalisation of cDNA microarrays, and analyses based on significance tests, controlling the false discovery rate, to find genes that were differentially expressed in hypothalamic samples from animals used as a model of human weight regulation. Our research collaboration in studying the bacterial composition of the digestive system has also been extended. Experiments show that the bacteria populations, and their metabolic products, change substantially in response to the macronutrient composition of the diet. We have begun developing mathematical models to further investigate the interactions between diet, bacteria, and their metabolic products such as butyrate, which are thought to play a role in the prevention of colon cancer.

BioSS manages its programme of applied strategic research in three broad themes:

- *statistical bioinformatics;*
- *systems & process modelling;*
- *statistical methodology.*

The research we carry out addresses generic issues encountered in our consultancy work that are not adequately addressed using standard methods. Each research theme is related to each of our four broad scientific application areas (below), demonstrating the wide applicability of BioSS research.

The [statistical bioinformatics](#) research theme addresses a wide range of modelling and data analysis problems that can be grouped under the six headings of genetic association, genomics, transcriptomics, proteomics,



metabolomics and regulatory networks. Our understanding of how important field traits such as disease resistance and yield are controlled has been greatly enhanced by mapping quantitative trait loci (QTLs) and establishing the relationship between traits and the QTLs. BioSS has produced the only available software, TetraploidMap, for mapping QTLs for tetraploid species such as potato. We have developed a simulation approach to allowing the effect of population structure to be taken into account in the identification of QTLs for barley. Also, we have been involved in mapping QTLs for soft fruit such as blackcurrant and raspberry. All of this work puts us in a strong position to help SCRI develop improved varieties of valuable crops.

The [systems & process modelling](#) research theme consists of methodological activities such as analysis, simplification and approximation of stochastic process models motivated by four classes of applications, namely: modelling large populations in heterogeneous environments; modelling risks to biodiversity in a changing environment; complex interactions in epidemic processes and Bayesian methods for decision support. This year has seen the formation of a new Centre of Excellence in Epidemiology, Population Health and Infectious Disease Control (EPIC), funded by the Scottish Government. This collaborative centre also incorporates five other internationally recognised research organisations, highlighting the strength of the Scottish research base in veterinary epidemiology. BioSS's role in EPIC is to develop, evaluate and apply methods of statistical inference for models of diagnostic testing and infection dynamics in animals. Given recent

outbreaks of foot-and-mouth disease and bluetongue, the establishment of the centre has been very timely, and it is hoped that EPIC will soon contribute to governmental, industrial and public understanding of issues relating to the control of epizootic and enzootic infections in animal production systems.

The [statistical methodology](#) research theme involves empirical modelling of data that are correlated due to the effects of space or time, extracting information from digital images, along with diverse methods such as compositional analysis and latent Gaussian modelling which need developing to resolve problems encountered in our consultancy work. One current project which has reached fruition this year has involved embedding the simplex, in which compositional data must lie, in an unconstrained space. Data are regarded as being generated from a Gaussian distribution in the unconstrained space, transformed so that points lying outside the simplex are mapped onto the simplex boundary and represent observed zeros in compositional space. This methodology has wide application to multivariate compositional data, including the analysis of daily food intake data which is both high-dimensional and contains a substantial proportion of observed zeros.

Further information about the work of BioSS can be found on the BioSS website [www.bioss.ac.uk](http://www.bioss.ac.uk). Details of particular interest include a wide range of examples of our work, a description of associated knowledge exchange activities and access to our software products.



# Reconstructing regulatory networks by integrating post-genomic data with biological prior knowledge

**Dirk Husmeier**

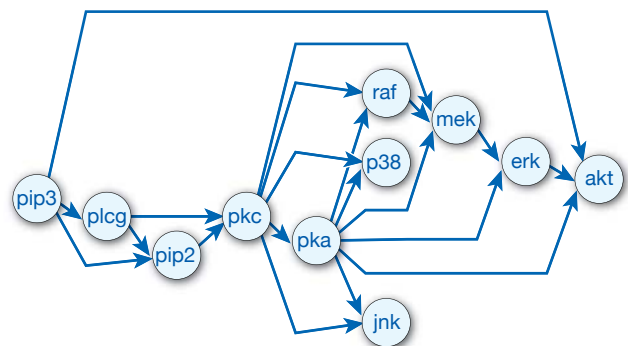
An important and challenging problem in systems biology is the inference of gene regulatory networks from high-throughput microarray data. Various machine learning and statistical methods have been applied to this end. An intrinsic difficulty with these approaches is that complex interactions involving many genes usually have to be inferred from sparse and noisy data. This leads to a poor reconstruction accuracy and suggests that the inclusion of complementary information and biological prior knowledge, related for instance to transcription factor binding locations in promoter regions or partially known signalling pathways from the literature, is indispensable.

We have developed a Bayesian approach to systematically integrate postgenomic data with independent sources of prior information. A hyperparameter that is automatically inferred when training the model determines the weight of the prior knowledge and trades its influence against the data. The approach is based on the methodology of Bayesian networks, reviewed e.g. in Husmeier et al. (2005). Details about the proposed scheme can be found in Werhli and Husmeier (2007).

We have evaluated the method on the Raf–Mek–Erk signal transduction pathway. Raf is a critical signalling protein involved in regulating cellular proliferation in human immune system cells. The deregulation of the Raf pathway can lead to carcinogenesis, and this pathway has therefore been extensively studied in the literature (e.g. Sachs et al., 2005). Figure 1 shows the representation of the currently accepted regulatory

network of 11 phosphorylated phospholipids (Pip2 and Pip3) and proteins (all other nodes), taken from Sachs et al. (2005). Several of the connections are direct enzyme–substrate relationships, like Pka to Raf, Raf to Mek and Mek to Erk. The edge between Pip3 and Plcg has a relationship of recruitment leading to phosphorylation. Some of the interactions shown are indirect and may involve specific phosphorylation sites of the signalling molecules. Our objective was to test if this regulatory network could be reverse-engineered from postgenomic data of the type available at a plant research institute like SCRI.

Sachs et al. (2005) have applied intracellular multicolour flow cytometry experiments. Each independent sample in the data consists of quantitative amounts of each of the 11 phosphorylated molecules, simultaneously measured from a population of over 5000 cells. This provides a rich data set from which Sachs et al. (2005) successfully reconstructed the gold-standard network of Figure 1 with Bayesian networks.

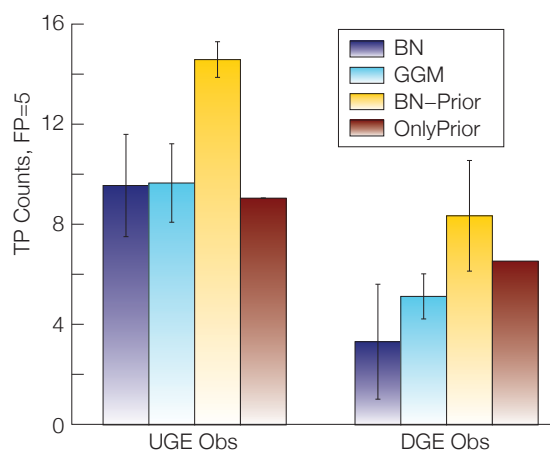


**Figure 1** Raf signaling pathway. The graph shows the currently accepted Raf signaling network, taken from Sachs *et al.* (2005). Nodes represent phosphorylated proteins and phospholipids, edges represent interactions, and arrows indicate the direction of signal transduction.

Unfortunately, the number of experimental conditions which can be explored with a microarray experiment at a plant institute is usually much smaller than at a medical research institute. To reflect this practical constraint we down-sampled the data from Sachs et al. (2005) to five non-overlapping sets of 100 experimental conditions. We then evaluated the accuracy achieved with the network reconstruction method, and



investigated to what extent the systematic integration of biological prior knowledge can improve the results. The source of prior knowledge we chose was the KEGG pathways database (Kanehisa and Goto, 2000), which represents our current knowledge of the molecular interactions and reaction networks related to metabolism, a variety of cellular processes, and different diseases. We extracted all pathways from KEGG that contained at



**Figure 2** Reconstruction of the Raf-Mek-Erk signalling pathway. The figure shows the means across five data sets of the number of true interactions inferred for a fixed number of 5 spurious edges. Each evaluation was carried out twice: with and without taking the edge direction into consideration (DGE and UGE respectively). The blue bars represent the results obtained from the data only, Bayesian networks (BN) and graphical Gaussian models (GGM); brown bars from the prior knowledge alone; yellow bars from the Bayesian approach, which systematically integrates the data with the prior knowledge from KEGG. The error bars show the respective standard deviations computed from the five replications.

least one pair of the 11 proteins/phospholipids included in the Raf-Mek-Erk pathway. We formulated our prior knowledge as a matrix containing the relative proportions of pairwise molecular interactions among all the pathways extracted.

The results are shown in Figure 2. The proposed Bayesian inference scheme clearly outperforms the methods that do not include the prior knowledge from the KEGG database. It also clearly outperforms the prediction that is solely based on the KEGG pathways alone without taking account of the cytometry data. The histograms indicate the accuracy one can typically expect to achieve with the amount of data included in our study, rising from a recovery of about 50% to 75% of the interactions in the pathway at a cost of incurring about 5% of false interactions.

This method is sufficiently generic that it can be applied directly to plant data in the study of plant regulatory networks.

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# Partnerships and Collaboration

SCRI's long established links with the Scottish Agricultural College were put on a more formal basis in May with the signing of a memorandum of understanding. A brief ceremony was held prior to the annual meeting of the Scottish Society for Crop Research.

The first months of the new partnership saw many encouraging outcomes. Recent collaboration on the development of diagnostics for potato diseases has led to a test for soil-borne pathogens, initially developed at SCRI, being further developed by SAC into a validated commercial proposition. SAC and SCRI will be collaborating in future to ensure that other relevant diagnostic tests are made available commercially through SAC.

Research on soils is taking into consideration the impacts of climate change on agricultural production, including the role of soil physical damage, biological

processes and extreme weather events on greenhouse gas production. SAC and SCRI soil scientists also collaborated with the Macaulay Institute on a RERAD funded project to identify 'Soil Quality Indicators'. By working together the group was able to encompass a much greater range of specialisms and to incorporate both strategic science and advisory expertise.

A Home Grown Cereals Authority for research on blending wheat was obtained during the course of the year. The aim is to investigate resilience, improved distilling quality and greater environmental stability. The project was derived from the previous work of Adrian Newton and Stuart Swanston on barley mixtures and wheat mixtures for distilling, and the earlier work of Bill Spoor and Steve Hoad on barley mixtures.



Professor Bill McKelvey, Chief Executive and Principal of SAC, Dr Keith Dawson and Professor Peter Gregory signing the Memorandum of Understanding.



SCRI's Director presents last year's annual report to Dr Mahmoud Solh, the Director General of the International Centre for Agricultural Research in the Dry Areas – ICARDA.



In January 2007 a group from SCRI, including Lesley Torrance, Pete Iannetta, Ian Toth and Geoff Squire, flew to Ås in Norway to sign a memorandum of understanding with Bioforsk – the Norwegian Institute for Agricultural and Environmental Research. (Photo: E. Fleistad/Bioforsk)

2007 also introduced a new relationship with Bioforsk – the Norwegian Institute for Agricultural and Environmental Research which is bringing new ventures and plans for joint research. In January an SCRI team including Lesley Torrance, Pete Iannetta, Ian Toth and Geoff Squire visited the academic complex at Ås in Norway for the signing of a memorandum of understanding.

SCRI has broadened its relationship with the European Alternative Splicing Network – EURASNET. The organisation brings together 30 leading research groups from eleven European countries as well as Israel and Argentina. Alternative splicing is an important factor in human disease and also in how plants grow and respond to changes in environmental conditions. SCRI contributes to this network through research conducted in a group led by Professor John Brown. An agreement has now been concluded under which SCRI will host and maintain the EURASNET website.

During 2007 SCRI staff were pleased to welcome no fewer than three, high level delegations representing the government of the People's Republic of China. In May, the Chinese Vice Minister of Agriculture visited SCRI:

together with other senior officials he discussed ways of strengthening UK – China links in agriculture and crop research. There were also visits by officials representing the various regional governments of China and by Dr Wang Baoqing, the Minister Counsellor for Science and Technology at the Chinese Embassy in London.

SCRI's links with China were further extended when Glenn Bryan from Genetics was invited to attend a UK–China Symposium on Genomics and Biodiversity during September. This symposium, jointly sponsored by the Royal Society and the Chinese Academy of Sciences (CAS), was held in the Wuhan Botanic Garden. Discussions were held on UK and Chinese research into the biology of the Solanaceae and possible areas of future collaboration were investigated. The Solanaceae – the nightshade family – contains a number of important food plants, such as potato, tomato, pepper and eggplant, as well as medicinal plants such as henbane. The Symposium ended with a 3-day field visit to the Xishuangbanna region of Yunnan province in Southern China, a region of extreme botanical diversity which is under severe threat from rapid expansion of iron mining and rubber-plantations.

# Research Services

**Communication and Information Services** At the start of the year, with the arrival of a new head of department, *Scientific Liaison and Information Services* became "Communications and Information Services" (CIS). Sarah Stephens undertook the role of Manager, Information Services and by year's end the former SCRI library had received a major refurbishment, including the provision of a lounge area. It is now designated the Information Centre.

Sharon Neilson had her role as Education Officer widened to include management of the many public and specialist events SCRI stages through the year from Open Days to our involvement in the Royal Highland Show.

Another major project for the CIS team was the construction of an entirely new SCRI website. By mid summer the site was "live" and met with critical approval. Lorraine Wakefield joined CIS as Information and Online

Services Officer. She embarked on a staff training programme to enable scientists and other colleagues to update their own staff pages and publications lists.

As well as the usual calendar of events during 2007, CIS supported the LEAF Open Farm Sunday event with marketing and publicity...arranged the Director's summer event for friends and stakeholders...and in December, staged a news conference in Edinburgh to launch Scotland's involvement in the 2008 United Nations Year of the Potato. To mark the event a booklet was published called "101 things you wanted to know about the potato...but were afraid to ask!"



SCRI news conference in Edinburgh to inaugurate the year of the potato.



Cereal Solutions – July 2007

**Estate Glasshouse and Field Services** Preparations for the building of a new Venlo glasshouse complex required the site to be cleared of a dozen large polythene and net tunnels which housed mainly soft fruit plants. These have been rebuilt in an adjacent field together with six new tunnels to replace space lost by the demolition of



an old unheated glasshouse. The new tunnels have a fully computerised irrigation system, which can vary the quantity and timing of water applied to suit the individual requirements of the different plant populations. This system was also extended to the newly created standing out ground. This consists of eight large bays which are completely enclosed by a 2-metre high wind break. Aluminium benching is to be installed as it released from life-expired glasshouses.



BBC 'River City's' Stephen Purdon – a special guest at the LEAF Open Farm Sunday.

Estate Glasshouse and Field Services staff were heavily involved in LEAF Open Farm Sunday. Team members operated the ever popular tractor tours linking various locations around the farm where displays, including floral attractant insect traps, global warming and minimum tillage, could be viewed. The new 'Living Field' Study Centre was put to work with many children's hands-on activities. Other events during the year where GFS staff were involved with the preparation and maintenance of the trials, as well as support on the day, were 'Cereal Solutions', 'Fruit for the Future' and 'Potatoes in Practice'.

**Finance and Corporate Services** Finance and Corporate Services had another busy year managing growth in turnover in excess of 2.5%. The eight members of staff provide assistance and advice to all staff members, working with research and support departments in delivering the service. The Contracts Division was established during the year to provide support with the pre and post award stages of external funding and it works closely with Procurement and Finance, the other divisions of Finance and Corporate Services Department in doing so.

Finance and Corporate Services is also responsible for ensuring compliance with Institute internal controls and continually reviews these controls, with support from internal audit to safeguard Institute assets.

In common with many other organisations involved in research, and in accordance with government recommendations, Finance and Corporate Services now prices external funding on a Full Economic Cost basis when the regulations allow this. The government objective is to ensure that the organisations involved in delivering this type of service are better-placed to sustain the infrastructure that supports the delivery of the service and by complying with the recommendation the department supports the activity of building up reserves to replace ageing assets.

To further support the Institute finances, Finance and Corporate Services endeavours to ensure that best value is achieved with regard to costs. The Procurement Division provides guidance and support in this area in accordance with Institute procedures.

The combined efforts of the divisions of Finance and Corporate services enable the production of annual accounts, monthly management accounts, budgeting, planning and risk assessment while simultaneously providing a point of reference for Institute staff on finance matters.

#### Health & Safety, QA and Environmental management

Joint exercises with Tayside Fire and Rescue and SCRI's first aid and breathing apparatus teams were carried out



An emergency exercise.



in February and September. The February simulated incident focused on rescue and first aid for people overcome by smoke. It was tied in with the annual exercising of the Business Continuity Plan and added a little realism to the role-play. The second simulated incident, in September, exercised the rescue and treatment of casualties contaminated with flammable and toxic chemicals. The exercises led to reviews of some SCRI procedures and were considered useful by both parties.

Audits of SCRI's Health and Safety, Quality Assurance and Environmental Management systems were conducted by UKAS-accredited auditors in April and November to assess our compliance with the standards OHSAS18001, ISO 9001 and ISO 14001 respectively. There were six minor corrective action reports in April, mainly relating to documentation, and one in November. BioSS was audited for the first time in April and was passed as compliant. There are certificates in force for all three standards for the Institute, MRS and BioSS.

This year has seen a significant overhaul of waste management with improved segregation. As well as recycling office paper, glass, aluminium cans, clean spent compost and cardboard we now separate out bare timber and a mixture of building rubble and non-recyclable compost. The latter mixture is used to seal the tops of land-fill sites which are no longer active, for which there is a cost saving. Anything not falling into these categories continues to go into land-fill.

**Human Resources.** During 2007 the HR department has been working on a variety of projects to deliver the HR Strategy 2006 – 11. Key pieces of work have included

- Delivering diversity awareness training for all staff
- Carrying out a review of the PPDR performance management system
- Identifying key skills required of managers
- Organising a change management training session for approximately 40 middle managers

The year has also involved the 5 HR staff in filling 30 posts across the organisation, and arranging events to meet the training and development for 220 staff.

In May 2007 the HR team was joined by Marelle Dalziel who had previously worked in human resources roles with SEPA and Napier University in Edinburgh.

The HR Committee met regularly during 2007 to review HR procedures as well as looking for alternative posts for staff affected by the end of funding streams. During the year approximately 30 people were affected with 25 staff being moved to work on new projects at SCRI.

**The Staff Association** has been very active providing social events for all members of the SCRI “family”. The Association has also continued to raise money for charity.

January saw a Burns-themed ceilidh at Bullionfield hall in Invergowrie with 75 people in attendance where one highlight of the evening was an address to the haggis by the Director!

The annual barbecue took place at the end of June and approximately 200 staff, family, and friends braved an early rain & hail storm but eventually enjoyed a lovely summer evening with fine cuisine grilled to perfection by enthusiastic senior staff.

At the end of November, a Craft Fair was held on site with stalls selling jewellery, cards, cosmetics, and home baked goods.

And at the close of the year a Christmas party entertained 39 young children who saw a display of magic tricks and enjoyed party games; they were also treated to some tasty refreshments, and a visit from Santa.

The Christmas lunch was attended by 70 staff members who enjoyed a fine meal put on by the restaurant staff and carol singing by the Invergowrie church choir. Fresh cut trees were available for staff to purchase before the Christmas break.

Other events that took place included 10 pin bowling and a craft night. Blood donor sessions were arranged and are coordinated to allow staff time to attend. The Association gives support to the golf, fishing, and football fraternities along with the corporate sports membership at Dundee University. Salsa, Indian head massage, Yoga and Tai Chi sessions have run throughout the year.

A new regular activity – Pilates – has started and has proved to be popular at lunch times.

Member's benefits include entry into a monthly draw to win meal & cinema vouchers. National Trust admission cards, and a Booker cash & carry card are available for use. We have a corporate subscription to "Which" magazine provided for the SCRI library and is also available to access online. Members are offered 25% off the full cost of any event/activity when they participate. Subscription fees remain at £1.50 per month and membership, currently around 200, is open to anyone

working at SCRI. The office bearers and committee are elected annually at the AGM where members are encouraged to nominate both local and national charities to be beneficiaries of the funds raised throughout the year. In 2007, three charities received £510 each. They are Cruse Bereavement Care Scotland, Dundee under 18's, and Fairy Box at Ninewells Hospital.

The Staff Association remains an integral part of SCRI, as it contributes greatly to the corporate well being and maintains a close working relationship with the Healthy Working Lives Initiative and the Staff Amenities group.

# Postgraduate Studentship Programme

**David Marshall, Gary Lyon and Craig Simpson**

This year has seen a further expansion in the student population at SCRI with the second full year of our Joint University Studentship programme. The total now stands at 27. This programme has now become a major feature of the research activity at SCRI. The institute welcomes both the diversity of the resulting student population and the valuable interactions with Universities across the UK that are already resulting in the development of new and exciting research opportunities. Recruitment for the 3<sup>rd</sup> year of the programme is now well underway and it is pleasing to see many new university partners joining in the scheme and a broad range of applicants from across Europe.

SCRI is now firmly established as an international centre of excellence for postgraduate training in plant and environmental sciences. Our organisation is, we believe, unique in the UK in providing a research environment which covers plant and environmental studies from the fundamental to the more applied aspects. This breadth provides a stimulating research environment which means that students are not only able to focus on their own research projects, using state of the art molecular and plant handling facilities, but are also able to experience and fully appreciate the wider context of their work. This is further developed through the close ties we have with key academic laboratories, major companies

such as those in the international plant breeding sector and key rural and environmental policy organisations in the UK and throughout the world.

As always the primary aim of the postgraduate training at SCRI is to equip the individual student with a wide range of modern, scientific skills whilst developing technical and intellectual competencies that can be applied in a range of scientific careers. We work closely with our university partners to monitor and support both delivery of this training and personal development to ensure that the individual student achieves their full potential and in so doing develops a comprehensive range of scientific and transferable skills. On graduation our students will be fully prepared to make a major contribution to the scientific base which is making an increasingly valuable contribution to the response of UK and international organisations to the consequences of changes in the rural landscape and agricultural systems brought about by climate change and increased demands on farming systems.

Students at SCRI are now registered at Universities across the UK; however a significant part of our postgraduate activities revolve around our well established partnership with the University of Dundee, and in particular with the Division of Plant Sciences, which is based at the institute. SCRI also hosts a number of





Michael Ravensdale (centre) and Rene Sonnenberg (second from right) meet Her Royal Highness The Princess Royal at the 2007 SABRI PhD student competition.

undergraduate and postgraduate student projects from many local universities and our staff contribute to UK and European courses. The relationship with Dundee University also includes a special arrangement whereby

all postgraduate students at SCRI can use facilities provided by the University of Dundee, including English language tuition, training courses, library, scientific facilities and counseling.

# The Scottish Society for Crop Research

**Bill Macfarlane Smith**

**Trustees:**

Professor J.R. Hillman  
Mr I.E. Ivory  
Mr A. Logan  
Mr J.S. Whitehead

**Chairman:** Dr S. Wale

**Vice- Chairman:** Mr A. Redpath

**Committee of Management:**

Dr K. Dawson  
Professor J.R. Hillman  
Mr I.E. Ivory  
Mr A. Logan  
Mr L.M. Porter  
Mr J.S. Whitehead

**Secretary:** Dr W.H. Macfarlane Smith

**Treasurer:** Dr N. Hattersley

**Registered Office:** c/o Scottish Crop Research Institute,  
Invergowrie, Dundee, DD2 5DA.

**Membership Numbers:** 300

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

- by organizing field walks and meetings 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 specialized 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 currently supports research on the effect of poor water distribution under irrigated crops of raspber-

ries, on the effects of adverse weather conditions on distilling quality in cereals, on the analysis of fifty years of meteorological data produced at the Scottish Crop Research Institute and on the further development of the Soft Fruit Gateway, a data resource on the diseases and other problems of soft fruit. Ongoing support is being provided for the consortium producing new varieties of raspberry, one of which, Glen Doll, is now available to growers. Financial support continues to be provided for a speaker at the Crop Protection Northern Britain Conference.

The Annual General Meeting was held on 29th May 2007, and was followed by the Invited SSCR Lecture which was given by Mr Tony Pexton, OBE, NSch, FRAGs, Chairman of the National Institute of Agricultural Botany, entitled "What do I, as a Farmer, expect from you as a Researcher".

SSCR has been reviewing its organisation to ensure compliance with the requirements of OSCAR and other such organisations, as well as taking account of the changing nature of research and the manner in which it is commissioned. One immediate consequence of this has been the broadening of the remit of the various Crop Sub-Committees, and in the case of the Cereal Committee, the change of name to the Cereal and Combinable Crops Sub-Committee, to allow it to embrace an interest in other crops such as oilseed rape.

The Society continues its major interest in Knowledge Transfer, which it achieves through the sponsorship and organisation of crop events, which are open to the general public as well as members, and half day technical meetings.

Of the former, 'Cereal Solutions', was held on 11th July 2007 and attracted 64 visitors, a further increase on the



SSCR Cereals Solutions.

2006 numbers. Among the demonstrations were plots of the Recommended List varieties of barley and wheat, current work on cereal genetics leading to improved varieties for brewing and distilling, work to reduce energy use and emissions of nitrogen in wheat production, low input trials of barley varieties grown as monocultures and blends including varieties old and new, genetic markers, research into *Rhynchosporium* and research on the genetics of barley and wheat to identify genes associated with mutation.

The 'Fruit for the Future' event held on 19th July 2007, attracted 90 breeders, growers, end-users and processors, again an increase on the previous year's excellent attendance. The latest research on raspberries, strawberries, blackcurrants, gooseberries and other soft fruits was displayed. Prospective new varieties of raspberry and strawberry were available for tasting assessment, with particular interest being shown in the new raspberry variety, Glen Doll, and other prospective varieties still in the course of development.

'Potatoes in Practice', the potato event supported by the Society, the British Potato Council, the Scottish

Agricultural College, CSC Crop Protection Ltd., and the Scottish Crop Research Institute, was held on 9th August 2007. The event again attracted a large number of visitors, so confirming its position as the largest outdoor display of potato cultivars, potato agronomy and related research on pests and diseases of the crop. The event featured a new, enlarged marquee with many more displays, and an enlarged outdoor display of potato crop machinery. Particular interest was shown in the new SCRI variety, Mayan Gold, which is being marketed by Greenvale AP.

The Potato and Soft Fruit Crop Sub-Committees held other half day meetings during the year to provide information to their relevant industries and to prioritise research for funding.

The Society continues to grow in size, with a number now taking advantage of the new category of Life Membership at a cost of £100. The Committee of Management is keen to encourage growers and processors to join the Society and to participate not just in the various crop-based meetings but also in the management of the Society and its various Sub-Committees.



# Mylnefield Research Services Ltd.

**Nigel W. Kerby & Jonathan B. Snape**

MRS, the commercial wholly-owned subsidiary of the Scottish Crop Research Institute (SCRI), was established in 1989 to enhance competitiveness, understand and fulfil the needs of industry and maximise the value of SCRI intellectual property and resources. The company has grown steadily and continued to benefit SCRI through annual Gift Aid and the provision of services, without any external financial assistance.

The Mission Statement of MRS is:

*To develop commercially the SCRI's scientific expertise, resources and intellectual property.*

**Finances** The income of MRS remained static at £1.97 million in 2006/2007 which was in line with our budget. MRS transferred £1.1 million to the SCRI Group, including £75k of Gift Aid. An additional £147k was retained as a provision pending a decision on the validity of one of our Plant Variety Rights. As in previous years, contract research (66%) was the biggest contributor to income, followed by lipid analysis (15%) and royalties (10%).

**Economic impact assessment** SCRI and MRS commissioned independent economists DTZ to undertake an economic impact assessment for the SCRI Group. This concluded that for every pound invested in the Institute by government, the UK economy benefited by £14. This is a truly impressive result and compares very favourably with other research institutes and universities and demonstrates the success SCRI, through MRS, has had in translating high quality basic research into added value products and services. In 2007 it was possible to see 7 named varieties (Mayan Gold, Lady Balfour, Claret, Anya, Inca Dawn, Vales Emerald, Vales Sovereign) of potatoes bred at SCRI on supermarket shelves in the UK, as well as one processed variety (Purple Star crisps). In addition SCRI soft fruit varieties find their way into a wide range of jams, juices, dairy products etc.

This result has been made possible by the long term relationships developed between MRS and its commercial customers.

**Glen Lyon** In early 2007, following a concerted effort by MRS to eliminate illegal propagation of the SCRI-bred raspberry variety Glen Lyon, a group of Spanish growers submitted a request to the European Plant Variety Rights Office to have the plant variety rights for Glen Lyon nullified. We are pleased to report that their nullity claim was rejected following a robust defence from MRS, without recourse to appeal. MRS will continue to vigorously defend SCRI intellectual property around the world and act on all reported cases of illegal propagation.



SCRI innovation MRS has taken to the market place.



**EnPrint®** In 2007, Dr Tim Daniell and Dr Dave Roberts received funding from Scottish Enterprise to further develop their environmental fingerprinting technology for the analysis of marine water samples. Following the successful conclusion of this project, MRS, with co-funding from Scottish Enterprise Tayside have invested in the development of this technology, with the aim of establishing a spin-out company, to be named EnPrint®, in late 2008. As part of this investment, Dr Rayne Longhurst has been employed to undertake business development and raise finance for EnPrint®. The technology has already attracted the attention of several major companies and other applications of the technology are being investigated.

**Licensing and IP asset management** MRS places significant emphasis on the protection of intellectual property generated by SCRI. Our IP portfolio is dominated by plant variety rights (55) but also includes three patents and five trademarks.

One of our commercialisation routes is through licensing and we currently have 411 licenses in 23 countries. MRS licences potatoes, forage and salad rape, turnip, kale, blackcurrants, blackberry, raspberry and strawberry varieties.

Since 1<sup>st</sup> January 2007, 4 potato varieties have been submitted to National List trials, 5 potato varieties were granted plant variety rights in Australia and 3 potato varieties were granted plant variety rights in Japan. In addition there were two applications for EU Plant Variety Rights, one raspberry, one potato variety. Two new varieties of blackcurrant, Ben Starav and Ben Klibreck, were commercialised in 2007.

**Analytical services** Mylnfield Lipid Analysis, under the leadership of Claire Traynor, had another successful year in 2007. A new GC-MS machine was purchased in June and this is now being used extensively to analyse oil seeds for a new multi-national customer. Ruth Razzo left MLA in 2007 and was replaced by Kris Devlin. Nicola Marquis spent 6 months working in MLA before returning to SCRI.

Dr Charlie Scrimgeour retired from SCRI in November 2007 but has been retained by MRS as a consultant

to advise on lipid analysis and stable isotope analysis. Lee Hunter received training in stable isotope analysis during 2007 and is now undertaking all the commercial analyses, a service that is now worth in excess of £70k per year and growing. With new appointments in analytical chemistry at SCRI imminent, this is an area of business activity we hope to grow in the coming years.

**Developing markets** MRS was instrumental in initiating discussions between China and the UK with the aim of establishing protocols whereby Scottish seed potatoes could be imported into China. This culminated in the lifting of the restriction for mini-tubers to be sent from the UK to China, an important first step in opening up a very large and growing market. Also in China, MRS, with the assistance of Dr Finlay Dale, established trials of SCRI-bred potatoes and germplasm. A cooperative Joint Venture ("Danasia") was established in China with the Danish company Berryfine, a Chinese fruit growing and marketing company, Beijing Jinaodun and the IFU (a Danish government venture fund). In return, for exclusive licensing of specific SCRI-bred soft fruit varieties, MRS will receive a 10% equity stake in Danasia. Significant areas of raspberry were planted in 2007 and will be marketed in 2008/2009 throughout China and the Pacific-rim.

**Knowledge transfer and exploitation** In 2007, SCRI benefited, through MRS, of being involved in several new initiatives, including the Tayside Knowledge Transfer Partnership, the Dundee Innovation Portal and Interface. These resulted in a Knowledge Transfer Partnership being initiated with the Edinburgh-based Nairns oatcake company and several other collaborations with local SMEs are being negotiated.

The Rainbow Seed Fund made its first investments in SCRI to develop the aberrant RNA technology developed by Dr Christophe Lacomme and Dr Krzysz Wypijewski, both in plant cells, and together with Dr Gyorgy Hutwagner of the University of Dundee, in animal cells. A full patent application was filed and work is due to commence on a Scottish Enterprise funded Proof of Concept project.

MRS also invested money in improving technologies for plant transformation based on the caspase expertise



of Dr Misha Taliani and Dr Brian Reavy. Initial results look highly promising and these methods are now being used by other research groups in SCRI as well as attracting interest from the agbiotech industry.

**CASE Studentships** MRS is the industrial partner in two CASE studentships. The first is with Dr Gary Loake of the University of Edinburgh and the second with Dr Ari Sadanandom of the University of Glasgow. Both these projects are generating potentially valuable intellectual property which will be evaluated and developed by MRS.

**Human resources** MRS values highly the skills and experience of all its employees and recognises their contribution, together with that of SCRI scientific and administrative staff, to company performance. MRS is committed to investing in training to ensure that all employees not only perform effectively and efficiently, but also gain long-term satisfaction from their work.

Prof. Bernard King stood down as Chairman of MRS after 2 years in the position and will stand down as a Director in April 2008. Keith Hopkins stood down as a Director of MRS in 2007 after more than 10 years service. We would like to take this opportunity to thank Bernard and Keith for their insight, support and encouragement over the years.

Peter Berry, formerly Chairman of the Crown Agents, took over as Chairman of MRS in September 2007 and brings a wealth of experience in commercialisation to the Board. In addition, Richard Buller, former Head of IP at Shell UK, joined the Board in September 2007 primarily for his in depth knowledge of intellectual property and related areas.

#### Acknowledgements

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

## The Mylnefield Trust

The Mylnefield Trust was set up in 2000. It has charitable status and its prime objectives are:

- To promote research and scientific work in the life, environmental and related sciences, in particular production of agricultural, horticultural and forestry crops, methods of limiting or eradicating pests and diseases, wood sciences and biomathematics, methods of increasing production or growth, improving cultivation and research into possible varieties.

- To promote the dissemination of such research.

To date the Trust has financially supported:

- A Research Incentive Fund.
- An Education Officer at SCRI.
- A hardship fund for an overseas student.
- Various research projects.
- Support for scientific publications.
- Postgraduate Award for Science.

The Trustees congratulate Michael Ravensdale as the first recipient of the Post Graduate Award.

Since its inception The Mylnefield Trust has supported projects and activities amounting to £113,000.

The Trust currently has funds of approximately £400,000, achieved mainly through donations from the profits of Mylnefield Research Services Ltd.

# Publications for the year 2007

Publications are classified in the following manner:

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

**Adam, M.A.M., Phillips, M.S. & Blok, V.C.** 2007. Molecular diagnostic key for identification of single juveniles of seven common and economically important species of root-knot nematode (*Meloidogyne* spp.). *Plant Pathology* **56**, 190–197. J

**Allcroft, D.J., Glasbey, C.A. & Paulo, M.J.** 2007. A latent Gaussian model for multivariate consumption data. *Food Quality and Preference* **18**, 508–516. J

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**Walters, D.R., Newton, A.C. & Lyon, G.D.** (eds). 2007. *Induced resistance for Plant Defence: A Sustainable Approach to Crop Production*. Blackwell Publishing, Oxford, 258pp. R

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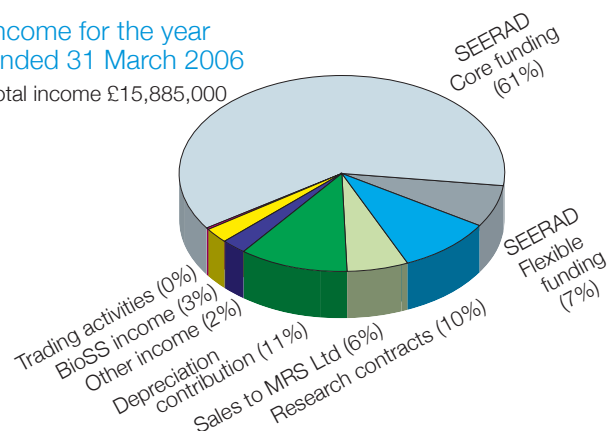


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- Zhan, J. & McDonald, B.A. 2007. Evolution of thermal adaptation in the wheat pathogen *Mycosphaerella graminicola*. *Population and Evolutionary Biology of Fungal Symbionts*, Ascona, Switzerland, 29 April–4 May 2007. P
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# Accounts

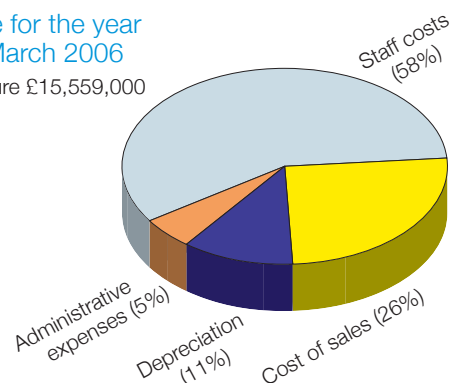
## Income for the year ended 31 March 2006

Total income £15,885,000



## Expenditure for the year ended 31 March 2006

Total expenditure £15,559,000



## Balance sheet at 31 March 2006

Total value £28,936,000

### Assets

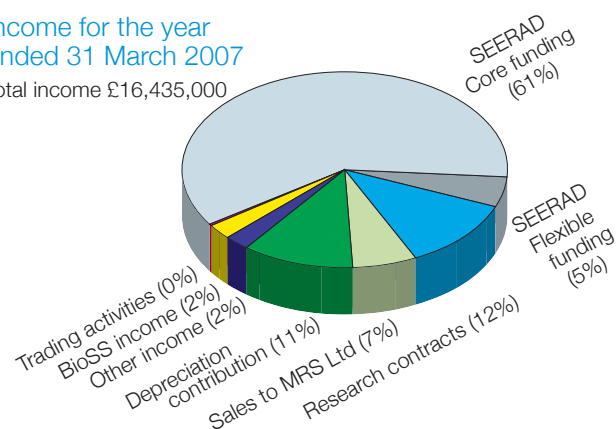
Fixed assets	95 %
Stocks	0 %
Debtors	5 %

### Liabilities

Capital reserve	85 %
Income & expenditure account	5 %
Current liabilities	10 %

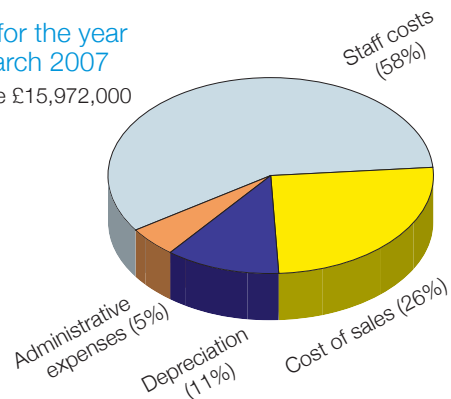
## Income for the year ended 31 March 2007

Total income £16,435,000



## Expenditure for the year ended 31 March 2007

Total expenditure £15,972,000



## Balance sheet at 31 March 2007

Total value £34,459,000

### Assets

Fixed assets	94 %
Stocks	0 %
Debtors	6 %

### Liabilities

Capital reserve	78 %
Income & expenditure account	6 %
Current liabilities	16 %

# Staff List

as at 1 October 2007

## Director

Director of Science Co-ordination

Director of Science Planning

Director of Finance and Corporate Services

P J Gregory BSc PhD Hon Dr (Debrecen) CBiol FIBiol FRASE<sup>4,12,13,14,15</sup>

H V Davies BSc PhD CBiol FIBiol<sup>1,2,4</sup>

D W Hopkins BSc PhD CBiol FIBiol<sup>16,17</sup>

N G Hattersley BSc PhD ACMA



## Genetics

R Waugh BSc PhD (Programme Leader)<sup>3,4</sup>

J Alexander BSc

M M Bayer MSc PhD

N Bonar HNC

A Booth HNC

C Booth BSc

J E Bradshaw MA MSc PhD<sup>3</sup>

R M Brennan BSc PhD

G J Bryan BSc PhD

X Chen BSc PhD

D Clark

G P Clark HNC BSc

J Comadran-Trabal BSc

M F B Dale BSc PhD<sup>3</sup>

D Davidson

L Donnelly

A Druka MSc PhD

I Druka

J D Fuller

S L Gordon HNC

J Graham BSc PhD

S F Gray BSc

B Harrower HND BSc MSc

P Hedley BSc PhD

I Hein MSc PhD

L Jorgensen HND

R Keith NEBS

D P King BSc

D J Leader BSc PhD

D Lewandowska BSc

M S Liney HND

J Lyon

N McCallum BSc

G McKenzie HND BSc

K McLean BSc

J McNicoll HNC BSc

M Macaulay HNC BSc

D F Marshall BSc PhD

H A Mathews

J Middlefell-Williams HNC

I R Milne BSc PhD

L G Milne BSc PhD

J Morris HND BSc

M Myles ONC

D Nwankwo BSc MSc

I Onyiah BSc MSc

G Ramsay BSc PhD<sup>3</sup>

L Ramsay BSc PhD

J Russell BSc PhD

S K Sharma BSc PhD

P D Shaw MSc

C G Simpson BSc PhD

K Smith DipHE

P L Smith BSc

G E L Swan

J S Swanston BSc PhD CBiol MIBiol

W T B Thomas BSc PhD

I M Tierney BSc MSc

A Wier

G Wilde

S L Williamson BSc

R N Wilson NCH

M R Woodhead BSc PhD

G R Young HNC

Dundee University

J W S Brown BSc PhD<sup>3,4,13</sup> (Principal Investigator)

Dundee University Group 1

A J Flavell BSc PhD (Principal Investigator)

J Grzebyta

N H Syed BSc PhD

Dundee University Group 2

C Halpin BSc MSc HDip PhD (Principal Investigator)

A Barakate BSc PhD

P Daly

Dundee University Group 3

G G Simpson BSc PhD (Principal Investigator)

J Marshall BSc DPhil

K Rataj

L Terzi BSc MSc PhD

Mylnfield Research Services

D Coyle

G Duncan BSc

L Ferguson

S N Jennings BSc

G Reid BSc



## Plant Pathology

L Torrance BSc PhD (Programme Leader)<sup>3</sup>

M Armstrong BSc PhD

A O Avrova BSc PhD

V C Blok BSc MSc PhD

P Boevink BSc PhD

J L Brierley BSc PhD

W Burry

M Burton

S N Chapman BSc PhD

D E L Cooke BSc PhD

G H Cowan HNC MSc

A Dolan HNC

E Douglas BSc

B Fenton BSc PhD CBiol MIBiol<sup>9</sup>

G L Fraser

E Gilroy BSc PhD

S C Gordon HNC<sup>3</sup>

D C Guy HND

N Holden BSc PhD

A M Holt

C Hornyik BSc PhD

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L Hutton HND

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K D McGeachy HNC

J McMillan

G L Malloch DCR BSc PhD

M Nasiadka

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P F Palukaitis BSc PhD<sup>1,5,10</sup>

A J Paterson HND

Y Pitkin BTEC HND

L Pritchard BSc PhD

E F O Randall MSc PhD

B Reavy BSc DPhil

W Ridley

A G Roberts BSc PhD<sup>3</sup>

J Shaw BSc

A Smith BSc

J N Squires BSc PhD

J A Stewart HND BSc

L Sullivan BSc

M M Swanson BSc PhD

M Talianky PhD DSc<sup>11</sup>

I K Toth BSc PhD<sup>6</sup>

E Warden ONC

S Whisson BSc PhD

N A Williams HNC

K M Wright MA PhD

K Wypijewski MSc PhD

V Young BSc

J Zhan BSc MSc PhD

A Ziegler BSc PhD

Dundee University

P R J Birch BSc PhD (Principal Investigator)

<sup>1</sup> Honorary Senior Lecturer in the University of Dundee

<sup>2</sup> Professor, Universities of Cordoba and Malaga

<sup>3</sup> Honorary Lecturer, University of Dundee

<sup>4</sup> Honorary Professor, University of Glasgow

<sup>5</sup> Adjunct Professor, Cornell University

<sup>6</sup> Honorary Lecturer, University of Aberdeen

<sup>7</sup> Honorary Fellow, University of Edinburgh

<sup>8</sup> Honorary Lecturer, University of Strathclyde

<sup>9</sup> Honorary Professor, Heriot-Watt University, Edinburgh

<sup>10</sup> Honorary Professor, Seoul Women's University

<sup>11</sup> Adjunct Professor, Moscow State University

<sup>12</sup> Visiting Professor, University of Reading

<sup>13</sup> Honorary Professor, University of Dundee

<sup>14</sup> Visiting Professor, University of Abertay, Dundee

<sup>15</sup> Honorary Fellow, Rothamsted Research

<sup>16</sup> Visiting Professor, University of Stirling

<sup>17</sup> Adjunct Professor, University of Canterbury New Zealand

<sup>18</sup> Special Professor, University of Nottingham

<sup>19</sup> Visiting Associate Professor, Cornelius University Bratislava





## Plant Products and Food Quality

D Stewart BSc PhD (Programme Leader)  
 M G Anderson MSc BSc  
 S C Conner BSc MSc CChem MRSC  
 D Cullen BSc PhD  
 H V Davies BSc PhD CBiol FIBiol<sup>1,2,4</sup>  
 G Dobson BSc PhD  
 P M Dobson  
 L J M Ducreux BSc MSc MPhil PhD  
 R D Hancock BSc PhD  
 R Hutchison  
 G J McDougall BSc PhD  
 D McRae ONC  
 N Marquis BSc

W L Morris BSc MSc PhD  
 P Neave NC  
 S D A Pont BSc  
 J Rauscher  
 H A Ross HNC PhD CBiol MIBiol  
 E Sabatinelli  
 L V T Shepherd BSc MSc PhD  
 T Shepherd BSc PhD  
 J A Sungurtas HND  
 M A Taylor BSc PhD  
 S R Verrall HNC  
 S Viverra BSc MSc

P G Walker HND  
 J F Wilkie  
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 F Gunstone BSc PhD DSc FRSE  
 L Hunter BSc  
 S Rowbottom ONC HNC BSc CChem MRSC  
 G Sawers BSc AMRSC  
 C Traynor BSc CChem MRSC  
 K Wood



## Environment Plant Interactions

P J White BA PhD (Programme Leader)<sup>18,19</sup>  
 G Banks BSc MSc  
 G S Begg BSc PhD  
 A G Bengough BSc PhD<sup>3</sup>  
 K Binnie BSc  
 A N E Birch BSc PhD CBiol MIBiol FRES<sup>3</sup>  
 L K Brown BSc  
 S Caul HNC  
 D Cullen BSc PhD  
 T J Daniell BSc PhD<sup>3</sup>  
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 L Dupuy MSc PhD<sup>3</sup>  
 M J Elliott BSc  
 F Falconer HNC  
 D S Feeney BSc<sup>3</sup>  
 L Ford BA  
 T S George BSc PhD  
 D C Gordon HNC  
 B S Griffiths BSc PhD<sup>3</sup>  
 P D Hallett BSc PhD

C Hawes BSc PhD  
 D W Hopkins BSc PhD CBiol FIBiol  
 R W Humphry BSc PhD  
 R G Hunjan  
 P P M Iannetta BSc PGCE(S) PhD  
 S N Johnson BSc DPhil  
 A J Karley BA DPhil  
 M Krol MSc  
 B M McKenzie BSc PhD  
 B Marshall BSc PhD ARCS  
 C Mitchell BSc  
 S M Mitchell BSc  
 R Neilson HNC MSc PhD  
 M Opik  
 D M Roberts HND BSc PhD  
 C M Scrimgeour BSc PhD<sup>3</sup>  
 G R Squire BA PhD  
 J A Thompson BSc  
 T Valentine BSc PhD  
 L Wiesel

J Wishart BSc PhD  
 G M Wright HNC  
 N Wuyts BSc MSc PhD  
 M Young HND MSc PG Dip IT  
[Mylnfield Research Services](#)  
 R E Wheatley BSc PhD  
[Dundee University Group 4](#)  
 H G Jones MA PhD FIHort (Principal Investigator)  
 I Leinonen PhD  
 R Ramsey BSc PhD  
 P G Schofield BSc PhD  
 L Spencer BSc  
 O Stasyk PhD  
[Dundee University Group 5](#)  
 J A Raven BA PhD HonPhD(Umea) CBiol FIBiol FRS FRSE  
 (Principal Investigator)



## Communication and Information Services

P Taylor (Head of CIS)  
 S Clifford  
 U M McKean MA DipLib

K Muir  
 S J Neilson DipBiolSci DipPollCon BSc  
 I R Pitkethly HND

S E Stephens BSc MA MCLIP  
 L Wakefield MA



## Information Technology

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

P J R Grimmond BA  
 R McCreary BSc

L A McGregor 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 MCIPD  
 M Dalziel MA PgDPM MCIPD  
 R G Davidson  
 M J De,Maine MBE BSc MPhil (Health and Safety Co-ordinator)  
 P Duncan

S Forsyth  
 K L Grant BA  
 B V Gunn  
 S Inglis  
 J Keith  
 C F Kydd FCCA  
 A Pack BA

W Patterson HND  
 M Pearson BSc  
 K Robb  
 A Sandilands  
 M Soutar  
 E L Stewart  
 L Young



## Engineering and Maintenance

---

S Petrie BSc (Head of Engineering and Maintenance)  
J Anderson  
D Byrne  
C Conejo  
G J E Ewart  
A G Fox  
D Gray HNC  
K A Henry

A Low MBE  
R D McLean  
I C McNaughton HNC  
E Millar  
G Pugh  
D J Redford  
G C Roberts  
J Rowe

W Scott  
B Semple  
B Ward



## Glasshouse and Field Services

---

P A Gill HND NEBOSH  
(Glasshouse and Field Services Manager)  
J Abernethy  
P Baird  
J R K Bennett  
J T Bennett  
E Caldwell  
C A Cuthill NC  
A G Dobson HNC HND  
I Fleming

J M Ford  
A C Fuller  
M A Grassie HNC BEd  
P Heffell ONC  
R Keith  
J Mason  
T A Mason NEBSM  
D I Matthew BSc  
A W Mills  
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 FIBiol (Managing Director)  
L Beaton HNC DMS MBA

M Beattie  
A Ross HNC CPP

J B Snape MA MSc PhD CBiol MIBiol MBA  
H Wilson



## 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)<sup>7,8,9</sup>  
S M Bierman BSc MSc  
S Catterall BA MSc PhD  
J M Dickson BSc  
D Glancy  
E M Heyburn MA  
D Husmeier BSc PhD  
M A M Kirkwood DA  
K Lin BSc PhD  
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 Polechova BSc MSc PhD  
A M I Roberts BSc MSc  
J Sales BSc MSc  
**West of Scotland Unit, Hannah**  
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  
D Lawson MSc  
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**  
J W McNicol BSc MSc (Head of Group)<sup>3</sup>  
C Alexander BSc PhD  
C A Hackett BA DipMathStats PhD  
D Lindner BSc  
K M MacKenzie BSc MSc PhD  
M Vignes BSc MSc  
F G Wright BSc MSc PhD



## Visiting workers

Name	Country of origin	Programme	Month/yr of arrival	Length of stay
K Arava	India	QHN	Apr-06	5 mths
S Arribat	France	QHN	Jun-07	2 mths
C Barnett	UK	EPI	Sep-07	7 mths
A Basha	India	PP	Apr-07	5 mths
B Begley	UK	PP	Sep-07	9 mths
D Berger	South Africa	PP	May-07	1 mth
D Bhattacharjee	India	PP	Apr-07	6 mths
M Bienvenu	France	QHN	Jul-07	5 mths
J Bisset	UK	EPI	Jul-07	1 mth
C Black	UK	EPI	Jul-07	1 mth
A Buddharaju	India	QHN	Apr-07	5 mths
T Canto	Spain	PP	Apr-07	3 mths
T Chan	China	EPI	Sep-07	6 mths
J Chaudhuri	India	PP	Apr-07	5 mths
B-N Chung	Korea	PP	Apr-07	6 mths
L Cobban	UK	EPI	Jul-07	1 mth
S Cobban	UK	EPI	Jul-07	1 mth
C Cognat	France	QHN	Jan-07	6 mths
A Confraria	Portugal	PP	Jun-07	2 wks
S Coulthurst	UK	PP	Jun-07	2 mths
A Custodio	Portugal	PP	Oct-07	3 mths
R De Jonge	Netherlands	PP	Apr-07	6 mths
P de Maayer	Belgium	PP	Aug-07	4 mths
S Devlin	UK	EPI	Jul-07	1 mth
M Elia	Spain	GEN	Jul-07	2 mths
A Flynn	UK	PP	Sep-07	9 mths
F Fraser	UK	EPI	May-07	4 mths
K Fuller	UK	GEN	Sep-07	1 wk
J Gandhi	India	GEN	May-07	5 mths
L Gomez Pando	Peru	GEN	Jul-07	1 wk
M Goubier	France	EPI	Apr-07	4 mths
W Griffiths	UK	QHN	Apr-07	2 mths
K Hanson-Pettengell	UK	EPI	Sep-07	6 mths
I Harrison	UK	DU	Sep-07	6 mths
G Hay	UK	DU	Sep-07	6 mths
D Holthusen	Germany	EPI	Jul-07	2 wks
K Juedtz	Germany	QHN	Feb-07	5 mths
M Keiller	UK	QHN	Sep-07	4 mths
L Kelly	UK	QHN	Sep-07	7 mths
N Kulkarni	India	QHN	Apr-07	5 mths
A Kumar	India	EPI	Apr-07	5 mths
A Landau	Argentina	GEN	May-07	3 mths
G Lau	Malaysia	GEN	Jul-07	4 mths
P Law	South Africa	PP	May-07	1 mth
J Lazano	Colombia	PP	Sep-07	2 wks
E Lebruin	France	PP	Jul-07	4 mths

Name	Country of origin	Programme	Month/yr of arrival	Length of stay
H Li	China	PP	Aug-07	1 mth
R MacAndrew	UK	PP	Sep-07	7 mths
D Mackay	UK	EPI	Sep-07	3 mths
J Nital	India	GEN	Jun-07	3 mths
L O-Hara	UK	GEN	Jul-07	2 mths
S Patel	India	EPI	Apr-07	5 mths
S Perron	France	EPI	Apr-07	3 mths
S Peth	Germany	EPI	Jul-07	1 wk
M Pfeiffle	France	GEN	Jun-07	1 mth
R Portieles	Cuba	GEN	Aug-07	3 mths
F Rakshshanderhoo	Iran	PP	Feb-07	5 mths
A Richardson	Australia	EPI	Sep-07	3 wks
E Robb	UK	EPI	Jul-07	1 mth
C Roger	UK	EPI	Sep-07	7 mths
C Rose	UK	EPI	Jul-07	2 mths
T Rotheray	UK	EPI	Jul-07	3 wks
L Russell	UK	DU	Jun-07	2 mths
E Sabatinelli	Italy	QHN	May-07	3 mths
C Sangani	India	PP	Apr-07	6 mths
S Scibetta	Italy	PP	Jul-07	1 mth
M Shepherd	UK	QHN	Sep-07	1 wk
T Shindo	Japan	PP	Jun-07	1 wk
V Singh	India	QHN	Apr-07	5 mths
R Solomon-Blackburn	UK	GEN	Oct-07	6 mths
J Stewart	UK	EPI	Sep-07	6 mths
L Sumei	China	EPI	May-07	3 mths
E Tataara	France	PP	Jul-07	1 mth
A Terranova	Colombia	PP	Jul-07	2 mths
P Torres	Spain	EPI	Sep-07	3 mths
R Ulloa	Argentina	GEN	May-07	2 wks
I Van Nugteren	South Africa	PP	Jun-07	2 wks
V Varma	India	QHN	Apr-07	5 mths
S Vivera	India	QHN	Jul-07	5 mths
N Voirin	France	GEN	Jun-07	1 mth
C Wagner	Germany	PP	Sep-07	1 mth
D Walker	UK	EPI	Sep-07	6 mths
E Wiik	UK	EPI	Jul-07	1 mth
C Willis	UK	DU	Sep-07	7 mths
J Yuste	Spain	EPI	Apr-07	3 mths
P Zaccharria	Germany	EPI	Jul-07	1 wk
A Zink	Germany	EPI	Jul-07	1 wk
P Barre	France	EPI	Sep-07	1yr
P Dennis	UK	EPI	Apr-07	3 yrs
S Hameed	Pakistan	PP	Dec-06	1 yr
B Centeno	Spain	EPI	May-07	2 yrs
A Kumar	India	PP	Apr-07	1 yr



## Honorary Research Fellows

Professor Richard Abbott BSc PhD  
 Dr Pamela Anderson PhD  
 Dr Hugh Barker BSc PhD  
 Professor Geoffrey J Barton BSc PhD  
 Dr Bill Belknap PhD  
 Professor Jill J F Belch MD(Hons) FRCP FAcadMedSci  
 Professor Jim Beynon BSc PhD  
 Professor Stephen Blackmore BSc PhD FLS CBiol FIBiol FRSE  
 Professor Mike Blatt BSc PhD FRSE  
 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  
 Dr Tim Close PhD  
 Professor John Crawford BSc PhD  
 Professor Michael C R Davies BSc DipTheol MPhil PhD CEng MICE FTG  
 Professor Pierre de Wit PhD  
 Professor Pete Downes OBE FRSE MIBiol PhD  
 Dr Jim M Duncan MBE BSc PhD  
 Dr Roger Ellis BSc PhD  
 Dr Andy Flavell BSc PhD  
 Professor Geoff Gadd BSc PhD DSc FIBiol FLS  
 Professor Mary Gibby BSc PhD FRSE FRSA  
 Professor Frank Gunstone BSc PhD DSc FRSC FRSE  
 Dr Claire Halpin BSc MSc H Dip PhD  
 Dr Linda Handley BA BEd MSc PhD  
 Professor Bryan Harrison CBE BSc PhD DAGFor FRS FRSE  
 Dr John Hayes BSc PhD  
 Professor Andreas Graner BSc PhD  
 Professor John Hillman BSc PhD DSc FLS CBiol FIBiol FIHort FCMi SHM FRAGS FRSE  
 Dr Pete Hollingsworth BSc PhD  
 Dr Steve Hubbard MSc DIC(London) DPhil (Oxon)  
 Professor Andrew Hudson BSc PhD

Professor Lindsey Innes OBE BSc PhD DSc FRSE  
 Professor Hamlyn Jones MA PhD FIHort  
 Dr A Teifion Jones BSc PhD  
 Professor Peter Langridge BSc PhD  
 Dr Gary Loake 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 FIBiol  
 Dr Donald K L MacKerron MBE BSc PhD  
 Dr Mike Mayo BSc PhD  
 Professor Tom Meagher BA PhD  
 Professor Andrew J Millar BA PhD  
 Professor Tim A Newson BSc PhD  
 Professor Hugh Nimmo MA PhD FRSA  
 Professor Karl Oparka BSc PhD  
 Dr Michel Perombelon MBE PhD MSc BSc Dip Agric  
 Professor Wayne Powell BSc MSc PhD DSc  
 Professor John Raven BA PhD HonPhD(Urmea) CBiol FIBiol FRS FRSE  
 Dr David J Robinson MA PhD  
 Professor David J Robinson BSc PhD  
 Mr Jean-Marc Rotsaert  
 Professor Karel Schubert PhD  
 Professor David M Spooner PhD  
 Professor Janet Sprent OBE BSc DSc PhD ARCS FRSE  
 Dr Alyson Tobin BSc PhD  
 Dr David L Trudgill MBE BSc PhD FIBiol  
 Dr Pieter van West MSc PhD  
 Professor Roberto Viola DipAgrSci PhD  
 Mr David Walker OBE  
 Dr Brian Williamson BSc MSc PhD DSc  
 Dr Roger Wise BSc PhD  
 Professor Iain Young BSc PhD



## Postgraduate students

Name	Programme	Project Title
Gillian Banks	EPI	Dynamics of feral oilseed rape populations and the impacts on associated insect communities.
Raymond Campbell	QHN	Genetics of carotenoid levels in potato tubers.
Emily Clark	EPI	Multi-trophic factors influencing aphid vector competence in a spatially heterogeneous environment.
Katy Clark	EPI	Does Mother know best? Is host plant selection by above ground insects influenced by below ground herbivores.
Emma Coates	QHN	Anti-cancer effects of soft fruit phytochemicals.
Jordi Comadran Trabal	GEN	Mapping adaptation of barley to drought environments (MABDE).
Sean Conner	QHN	Metabolic profiling of potato ( <i>Solanum tuberosum</i> ).
Suzanne Donn	EPI	Molecular ecology of soil nematode communities.
Martin Elliot	EPI	On modelling GM oilseed rape populations.
Dominique Hardy	PP	Biofilm formation by <i>Pectobacterium atrosepticum</i> on potato tubers.
Gerald Hochshartner	GEN	Application of a novel snoRNA marker system in plant evolution and systematics.
Severine Grouffaud	PP	Translocation of <i>Phytophthora</i> effectors and their manipulation of host plant disease resistance.
Louise Kasprowicz	PP	The population dynamics and ecophysiology of the peach-potato aphid <i>Myzus persicae</i> .
Jennifer Kennedy	EPI	AM fungi in agriculture.
Susan McCallum	GEN	Linking phenotype to genotype for fruit quality traits in raspberry.
Sandy MacDonald	GEN	Regulatory pathways involving iron acquisition in <i>Pasteurella multocida</i> A:3, their role in pathogenesis and relevance to disease mechanisms in <i>Pectobacterium atrosepticum</i> .
Tim Miller	PP	Metabolic and proteomic profiling of the interaction between plant hosts and root knot and cyst nematode endophytes.
Carolyn Mitchell	PP	Cane fruit: Novel approaches for ICM in fresh and processed crops.
Lucy Moleleki	PP	Characterization of the interaction between type three secreted proteins in <i>Pectobacterium atrosepticum</i> and its host plant <i>Solanum tuberosum</i> L.
Juan Gonzalo Morales Osorio	PP	Mechanisms of virulence and avirulence in the biotrophic interaction between potato and the late blight pathogen <i>Phytophthora infestans</i> .
Michael Ravensdale	PP	Unravelling the regulatory mechanisms involved in the production of coronafacoyl phytotoxins and other pathogenicity determinants in <i>Pectobacterium atrosepticum</i> .
Christelle Robert	BioSS	Elucidation of the regulatory binding sites in bacterial genomes.
Rosalind Taylor	PP	Ubiquitin-proteasome directed proteomic approach to dissect biotic stress signalling in plants.
Maja Thorsen	EPI	Biological mechanisms involved in stabilizing sandy soils of the Machair.
Stefanie Vink	EPI	Functional soil ecology and conservation in the Machair in relation to changing land management.
Tobias Wojciechowski	EPI	Root development in semi-dwarfing lines of wheat and barley.
Han Xiao	QHN	Function of polyphenols in chemoprevention.



# SCRI Research Programme

ongoing as at 1 October 2007

The research programme is commissioned by RERAD and a variety of other funders. The list contains the body that awarded this 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/589/02	Novel methodologies and tools for the analysis of germplasm collections.
SCR/842/02	Elucidation of regulatory and signalling networks that control bacterial disease development.
SCR/908/03	Post-genomic analysis of <i>Erwinia carotovora</i> virulence responses in <i>in vitro</i> and <i>in planta</i> environments.
SCR/910/04	The genetics of gene expression in barley.
SCR/913/05	Characterisation and development of gene silencing in <i>Phytophthora infestans</i> for high-throughput determination of gene function.
SCR/915/06	Limiting the risk from <i>Phytophthora idaei</i> to the Scottish raspberry industry.
SCR/918/07	Genomics-assisted dissection of barley morphology and development.
BSS/842/04	Elucidation of regulatory and signalling networks that control bacterial disease development.
BSS/843/04	Control of pulmonary adenocarcinoma (jaagsiekte) in the Scottish sheep flock.
BSS/845/06	Epidemiology, population, health and infectious disease control.

## External research contracts

Agro-Transfert	Development of MAPP for the French market.
Avebe	Development of OptiNut Version 1.0.
BBSRC	Visualisation and modelling of plant morphogenesis: a dynamic toolkit for cell expression and fluorescent cell reporters in roots.
BBSRC	Visualisation and analysis of biological sequences, alignments and structures.
BBSRC	Targeted induced mutation discovery in barley.
BBSRC (CSI)	Optimising wheat grain shape for improved processing quality.



BBSRC (CSI)	Exploiting the <i>Phytophthora infestans</i> genome to identify gene targets for sustainable potato protection.
BBSRC (CSI)	The establishment and application of a forward genetic resource for the development of efficient breeding strategies in grass and cereals.
BBSRC LINK	Association genetics of UK elite barley.
BBSRC LINK	Role of inoculum sources in <i>Rhynchosporium</i> population dynamics and epidemics on barley.
BBSRC LINK	Testing trophic-functional relationships for modelling farmland diversity and functional dynamics.
BBSRC (via John Innes Centre)	Chemical interrogation: a new 'systems' approach to starch metabolism in germinating barley seeds.
British Council ARC Programme	A physically based understanding of crack genesis in soil and the impact of land management and biological processes.
British Potato Council	Improving decision-making for the management of potato disease using real-time predictive diagnostics.
British Potato Council	Independent variety trials.
British Potato Council	Survey of GB blight populations.
British Potato Council	Integrating quality trait development with large-scale gene expression analysis in potato.
CIMMYT	Genomic dissection of tolerance to drought stress in wild barley.
Commercial	Brassica breeding.
Commercial	Potato breeding.
Commercial	Molecular pathology.
Commercial	Blackcurrant breeding.
Commercial	Lipid analysis.
DEFRA	Crop physiology.
DEFRA/HGCA	GREENGRAIN: Genetic reduction of energy use and emissions of nitrogen in cereal production (LINK).
DEFRA/SEERAD	Integrated pest and disease management for high quality protected raspberry production.
EPSRC	Novel approaches to networks of interacting autonomes.
EU	ALARM project.
EU	SIGMEA: Sustainable introduction of GM crops into European agriculture.
EU	SAFEFOODS: Promoting food safety through a new integrated risk analysis approach for foods.
EU	BIOEXPLOIT: Exploitation of natural plant biodiversity for the pesticide-free production of food.
EU	Improving seed quality in cereals by manipulating gene expression and partitioning.
EU	EURASNET: European alternative splicing network.
EU	EU-SOL: High quality solanaceous crops for consumers, processors and producers by exploration of natural biodiversity
EU	DEVELONUTRI: Development of high throughput approaches to optimise the nutritional value of crops and crop-based foods.
EU	BARLEYBREAD: European guideline for healthy high fibre/low salt baking process based on the use of European barley.
EU	GENBERRY: European small berries.

EU Marie Curie	Training site in plant virology.
EU Marie Curie	GENFUNDIV: Linking the genetic and functional diversity patterns of arbuscular mycorrhizal fungal communities in disturbed and undisturbed environments.
EU Marie Curie	Role of arbuscular mycorrhizal fungi on the accumulation of radiocaesium by plants.
European Science Foundation	Exploiting genomics to understand plant–nematode interactions.
Food Standards Agency	Development of unified data models and data pre-processing strategies and the generation of meaningful, standardised statistical analyses of metabolome variability in crop plants.
Food Standards Agency (via John Innes Centre)	Development of a standard, validated procedure for the isolation of transgene flanking regions in GM crops and detailed analysis of transgene insertion.
HDC/SEERAD/Commercial	The breeding and commercial development of new raspberry varieties.
Horticultural Development Council	Developing techniques to manage raspberry leaf and bud mite in tunnel produced raspberry.
INRA	Global change at the microbial scale – effects of climate change on microbial decomposition and modulation of physical structure of soil.
MacRobert Trust	Biodiversity in Tayside.
Ministry of Spain	Study of the effect of the treatment with methyl jasmonate on the bioformation of chiral volatile compounds in vegetal foods.
NERC (via University of Stirling)	Microbial diversity in Antarctic soils.
Rainbow Seed Fund	A platform technology for high throughput gene knockdown based on aberrant RNA technology (ART).
Royal Society	Molecular basis of pathogenicity in the pine nematode <i>Bursaphelenchus xylophilus</i> .
Royal Society	Characterisation of plant genes that confer disease resistance to oomycetes.
Royal Society	Genetic control of lateral root development stimulated by rhizosphere nematodes.
Royal Society	Transcript profiling of meristem activation in potato using the POCl microarray.
Royal Society of Edinburgh	RSE/Scottish Executive Personal Fellowship.
Rural Development Administration of Korea	Development of manipulation techniques of plant viruses for the development of multiple virus resistant horticultural crops.
Scottish Enterprise	Genetic fingerprinting for environmental monitoring.
Scottish Enterprise	Additive-free treatments for shelf-life extension of minimally processed foods.
SEERAD/BPC/Commercial	Understanding and improving flavour characteristics of potato (LINK).
SEERAD/HDC	Developing a marker-assisted breeding toolkit for premium sensory characters in raspberries.
SHEFC	Scottish Bioinformatics Research Network (SBRN) maximising bioinformatics infrastructure for Scottish Health, Agriculture and Industry.
Stirling University Innovation Park Ltd	Increased efficiency of plant transformation and regeneration.
University of Nottingham	Biofortification of wheat with selenium through agronomy and genotype selection to increase human dietary intake (LINK).
USDA	Contribution to biological, virulence and molecular characterisation of <i>Globodera pallida</i> from Idaho.
Waste and Resources Action Programme	Support for trials of composted products in added value markets.

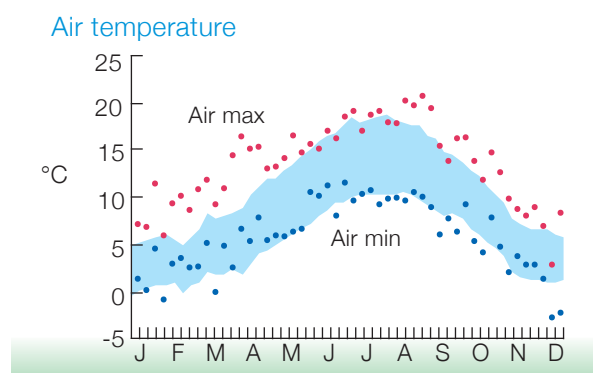
# Meteorological Records

2007

**Marion Grassie**

**General** The very successful LEAF Open Day in June gave members of the public the opportunity to visit SCRI's meteorological station to see how weather is observed and recorded. They were able to look at a range of weather measuring and recording instruments and talk to SCRI's climatological observers.

**Temperature** In 2007 all months showed average maximum temperatures higher than the Long Term Average (LTA), with the exceptions of June at 16°C (LTA 16.8°C) and July at 18.5°C (LTA 19.0°C). Most significant figures were observed in January at 9.0°C (LTA 5.9°C), the highest since 1989; and April at 15.3°C (LTA 10.9°C), the highest on our records. Highest maximum air temperatures recorded on individual days reached 21.8°C, 22.0°C and 24.2°C for July, August and September respectively; and 20.9°C in April.

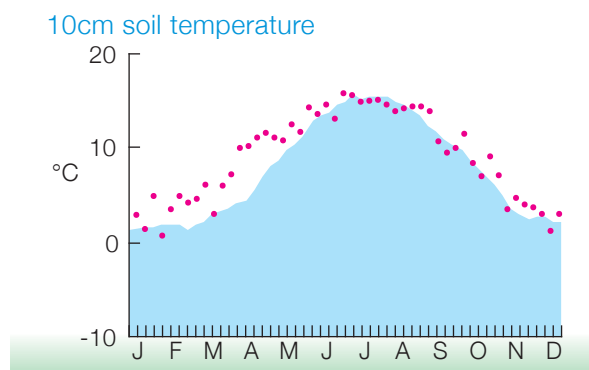


Average minimum temperatures were also generally higher than typical, exceptions being July, August, September and December which were all slightly lower than their LTA. The total days per month with air temperature <0°C were all below the LTA except December, which had 18 (LTA of 10).

Although only June and July escaped, the number of days with frost was lower than LTA for most months.

Blue areas on figures indicate long term average 1961–1990

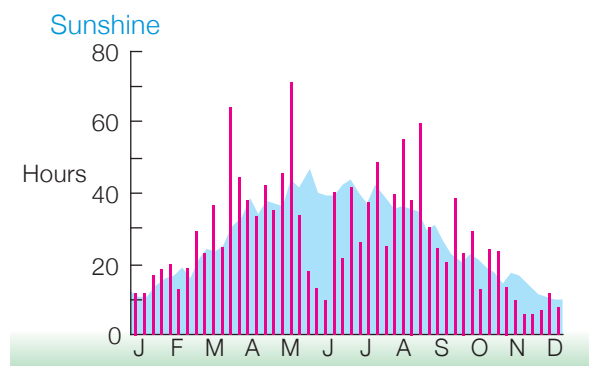
Exceptions to this were May, December and in particular August (with 6 against the expected 1 – the highest on our records); and September (with 8 against the expected 3 – second highest).



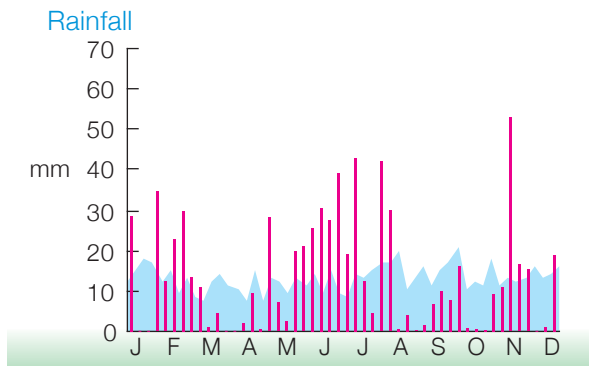
Mean soil temperatures were also higher than the LTA, except from June to August where a slight drop in temperature was recorded at higher levels.

Mean soil temperatures were also higher than the LTA, except from June to August where a slight drop in temperature was recorded at higher levels.

**Sunshine and Solar Radiation** Sunshine figures were fairly mixed with a total of 1428.1 hours, close to the LTA of 1411.6 hours. Notable were April with 194.4, 50







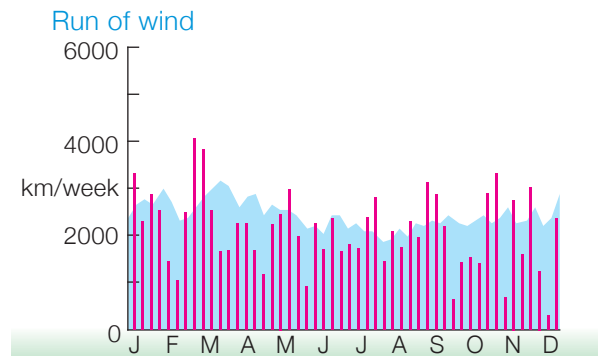
hours more than the LTA; and June, with 90.3, 80 hours less than the LTA (lowest since 1954).

Solar radiation values were not exceptional, although 8 months had higher than normal readings.

**Rainfall** As with 2006, rainfall was higher than normal, the annual total reaching 741.5mm as compared to the LTA of 664.5mm. Most notable being June and July with 104.6mm and 117.3mm respectively, both of which had more than double the expected rainfall. In contrast, April recorded 11.4mm, a quarter of the LTA of 44.6mm.

**Wind** On the whole, wind speeds were unremarkable. Exceptions being 9 recorded days of gale (mean wind speeds of 34 knots+): 4 in mid-January, 3 in mid-March, 1 in May and 1 in December.

**Knowledge Exchange** In December, the SCRI website weather pages went live. These consist of a general overview page and a data page. The overview page briefly explains the value of meteorological data, the use



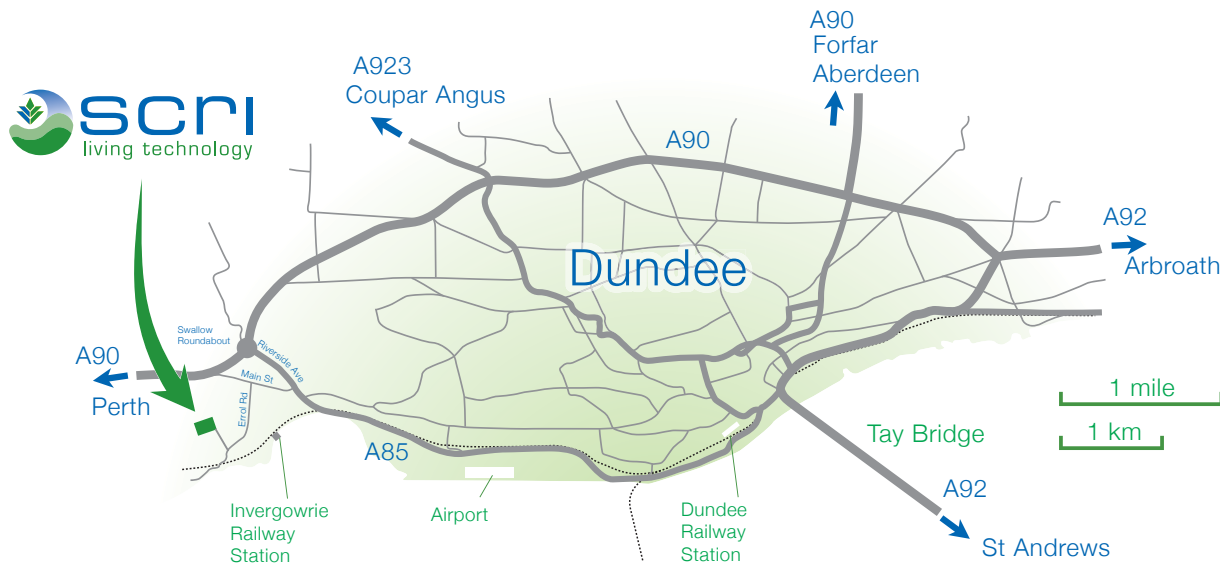
it is put to by staff within and by bodies or individuals outwith SCRI, and the type of data available. This can be viewed at <http://www.scri.ac.uk/knowledge/weather>. The weather data page contains a selection of weekly averages and totals for the most recent four weeks on a rolling basis and is updated weekly. It also provides monthly averages and totals for the current year, updated at the end of each month. This information can be accessed at <http://www.scri.ac.uk/knowledge/weather/data>.

The weather data collected at SCRI is passed on to the UK Meteorological Office. It is also shared with the community via the local media. The Dundee Courier and Dundee Evening Telegraph publish a monthly summary of the weather statistics which is provided by SCRI's meteorological observers. We are also contacted by the media on a regular basis during extreme weather conditions to provide meteorological context. The weather station and its observers have also featured on local television news bulletins.

## Directions to SCRI

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

It is located at Invergowrie 6km 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 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 Swallow roundabout. 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 39, 54 and 16 bus routes. The bus stop is on Errol Road and there is a footpath to SCRI between the houses.

Dundee Travel Information [www.dundeetravelinfo.com](http://www.dundeetravelinfo.com)

Stagecoach Bus [www.stagecoachbus.com](http://www.stagecoachbus.com)

### By train

Regular trains from Glasgow, Edinburgh, London and other UK cities run to Dundee.

National Rail Enquiries [www.nationalrail.co.uk](http://www.nationalrail.co.uk)

### By air

Air France runs regular flights between London City and Dundee airports as part of its CityJet service (previously operated by ScotAirways).

Air France [www.airfrance.co.uk](http://www.airfrance.co.uk)

# Website

The SCRI website was designed, constructed and successfully launched in August 2007.







