



Annual Report 2008



Governing Board

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Introduction

Peter J. Gregory

Our focus for the first half of 2008 took over from where 2007 had left off, with widespread newspaper comment on rising food prices and a realisation that the food system and cheap food could, perhaps, no longer be taken for granted. *The Economist* magazine of 19-25 April suggested a “tsunami” affecting world food security, and there were riots resulting from increased prices and shortage of supplies in several cities worldwide. A variety of reasons, many operating on different timescales, were given for these increased

food prices including speculation, the falling value of the US dollar, increased demand for grains, export bans on selected foodstuffs, inadequate grain stocks, higher oil prices, poor harvests and the use of crop lands for the production of biofuels. Whatever the reasons, food policy and food security are now back on the UK agenda in a big way. We contributed material to the launch of a Food Policy by the Scottish Government in June 2008, and there is growing interest in improving the diet and health of the Scottish population. There is



Peter Gregory

increasing evidence that eating a wide variety of plants plays a vital role in human health and our research on Plant Products and Food Quality is increasingly being sought and used for policy and by commercial customers. Throughout the year I attended a range of meetings in London seeking to support policy development in the area of UK food security and research priorities are starting to emerge in which SCRI's research will play an important part.



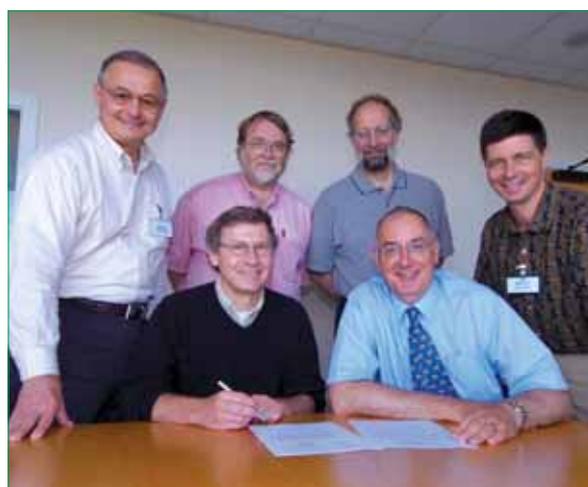
Left to right: Madam Ma Shuping, Chinese Ministry of Agriculture, Pete Wishart MP and Dr Pamela Anderson, Director-General CIP, Peru,

2008 was the UN International Year of the Potato and we celebrated this in August with a conference in Dundee on Improving International Potato Production. It was a great success with visitors from China, India, Peru, the Netherlands and UK businesses all sharing their insights. Potato is now the world's third most important crop in terms of production after rice and wheat and it was gratifying to see the SCRI Group's research and breeding contribution placed in an international context. Potato is increasingly being seen as a means to improve livelihoods in rural communities close to growing towns and cities in Africa because there is demand for the crop and the produce can be sold for cash. Production is increasing rapidly in some regions but there are major problems with diseases. Coincidentally, the year ended with our long-term partner Greenvale AP winning the Tesco Fresh Produce Variety of the Year award for the potato variety Vales Sovereign bred at SCRI. They, and we, have a winner which is starting to establish itself as a major variety in the UK.



The Tesco Fresh Produce Variety of the Year bred at SCRI.

SCRI has for many years benefited from numerous links to the international scientific community but we have placed even more emphasis on this recently. To mark this there is a new section of this report on SCRI Worldwide, and during 2008 we entered into some new agreements with institutions overseas. We now have a formal link with Michigan State University with whom we share interests in potato and soft fruit breeding as well as plant-soil interactions. MRS became a partner in Danasia in China, a company that will use our varieties of raspberry and blackcurrant in a venture to increase production and consumption initially in the Beijing area. Closer to home we shall cooperate with ILVO in Belgium, especially in areas of plant pathology and food quality. We were very pleased to receive the Governing



Signing a Memorandum of Understanding with Michigan State University.



The MoU being signed between SCRI and ILVO

Board of Bioforsk, Norway, with whom we are working ever more closely in topics related to sustainable production research.

Outward-looking research scientists collaborating with the best internationally and shaping the research agenda are essential components of research excellence. Our research quality and outputs were reviewed by external panels during the year in two exercises. Firstly, the major Scottish Government programmes of research in which SCRI participates (Profitable and Sustainable Agriculture - Plants) with SAC (Scottish Agricultural College) and The Macaulay Institute were reviewed by sizeable external panels to ensure that they are on target to deliver the outcomes commissioned by 2011. The preliminary feedback was very complimentary about the quality and quantity of what had been achieved, and there were few concerns about the direction and outcomes. Internally, the Governing Board has instituted a rolling programme of reviews of the science programmes and in 2008 it was the turn of Genetics to be scrutinised by an international panel of experts in the field. Their report was highly complimentary about the international excellence of the science being undertaken and the demonstrable leadership exhibited by staff in the programme in their various fields of study.

As ever, the year produced new and exciting results from our research programmes. Green fluorescent protein isolated from jellyfish has been widely used by plant and soil scientists to study the movement of proteins in living plant and microbial cells. However, these fluorescent protein markers are quite large hence

they cannot be introduced easily into all cell types. In particular, they have limited use with viruses because movement within a plant is restricted. Our Plant Pathology programme has worked with scientists at Glasgow and Edinburgh universities to develop a much smaller fluorescent protein based on the light, oxygen or voltage-sensing domain of the blue-light receptor in plants, phototropin. Use of this new protein means that infection processes involving viruses can now be studied more readily because cell to cell movement is not artificially constrained by the size of the accompanying fluorescent protein. So, we now have a new tool available to study cellular processes especially in systems where genome size or protein shape was previously limiting. This research involved the “shuffling” of DNA, but more conventional work with DNA to ‘fingerprint’ microbes in seawater, and freshwater has reached a point where it will form the basis of a new spinout company from SCRI. EnPrint will offer a service for the microbiological analysis of seawater, facilitating compliance with recently approved EU legislation on water quality.

In our Environment Plant Interactions programme, techniques have been developed in collaboration with the University of Nottingham, the Nottingham Arabidopsis Stock Centre and Warwick HRI for genome-wide analysis of transcription in several plant species using commercially available nucleotide microarrays. The results suggest that many of the differences in gene expression between plant species, ecotypes and even between specific cell-types, have no adaptive significance and reflect ancestral plasticity and founder effects. In short, changes in the transcriptome cannot be assumed to be adaptive.

Determining the genetic sequence of plants and pathogens is increasingly providing novel insights into the behaviour of crop plants and is at the heart of much of our biology. In our Genetics programme, work has started with partners in Ireland, Imperial College and the University of Dundee to sequence chromosome 4 as a contribution to the International Potato Genome Sequencing Consortium. This complements existing work to sequence chromosome 4 of the tomato and the wide-ranging genotyping of barley. For example,



Professor Bernard King (right) hands on the Chairmanship of the SCRI Governing Board to Peter Berry (left).

each line in the Bowman collection of barley mutants developed by Jerry Franckowiak of the University of North Dakota has been genetically characterised. The results allow the location of the mutated genes to be defined, assessment of the distribution of genes in relation to a marker map, and the success of subsequent rounds of backcrossing in eliminating donor genes.

On the European scene, colleagues in Plant Products and Food Quality have played a key coordination role in the EU Integrated Project 'Promoting Food Safety through a New Integrated Risk Analysis Approach for Foods' (SAFE FOODS). This project has been at the forefront of assessing the potential value of advanced, broad scale analytical 'omics' technologies within a risk assessment framework to determine the safety of foods. Using potato and maize as model crop species, the project has shown that variation in gene protein and metabolite expression is large with respect to genotype, growing site and season, and even crop management practices. Any differences between GM and non-GM crops tested were dwarfed by comparison. These approaches could therefore be used to benchmark any measured differences in a particular crop against the extent of acceptable variation within a framework of 'safe' use.



Farm Manager Euan Caldwell receives the Director's Award 2008.

We said farewell to longstanding Member and Chair of the Governing Board, Bernard King, during 2008 and welcomed Peter Berry as his replacement. The Board have supported me in my work to make real the First Minister's announcement in January that SCRI and The Macaulay Institute would be encouraged to come together in a single body. The Director of The Macaulay Institute, Richard Aspinall, and I have drawn up a draft science remit for the new institute and work continues with the Scottish Government to devise a plan that will be acceptable to the Boards of both institutes. As we look forward, this potential new structure for our research will clearly influence the scope of our scientific endeavours.

The Director's Award for 2008 was made to our Farm Manager Euan Caldwell for his outstanding contribution to the life of the Institute, and particularly for his rapid improvisation of arrangements to ensure that Potatoes in Practice did not become Potatoes in Mudbath during a dreadfully wet August.

I hope that you will enjoy reading about the excellence of our research and its communication to numerous audiences.

P J Gregory

10 January 2009

SCRI Worldwide

Scientific research and SCRI's reputation transcend national borders. Excellent research at SCRI involves partners across the globe and from university, business and research institutes. The support from funding bodies and the scientific publications produced by SCRI scientists bear witness to our status as a world class research institute.

The countries of joint authors in scientific publications are shown in Fig.1. There were 266 collaborators in 27 European countries excluding the UK. Large tracts of the world are covered from Argentina to Japan, New Zealand to Canada, and South Africa to Estonia. Collaborations exist with China and India as well as smaller economies such as South Korea, Mozambique, Syria and the Philippines. Research is also carried out in Antarctica. All aspects of SCRI research are represented.

Over recent years SCRI has built up a portfolio of Memoranda of Understanding (MoU) with organisations to support collaboration. These cement previous relationships and provide the framework for collaborative research, the opportunity for joint funding applications,

exchange of staff and information for training as well as research, and the organisation and sponsorship of seminars and conferences.



Chinese delegation visits Potatoes in Practice

SCRI and MRS have a long history of collaboration with China at the levels of national and state government, specific research institute and individual researcher. SCRI's Improving International Potato Production conference, held to mark the UN International Year of the Potato, attracted a high level delegation from China. While the delegates were in Scotland they visited SCRI and attended Potatoes in Practice. Negotiations to allow



Figure 1 Geographical location of joint authors in publications listed in Web of Science 2005 – April 2008.

the export of Scottish seed potato mini tubers to China has been facilitated by SCRI and MRS. There is an MoU in the field of potato research with Sichuan Academy of Agricultural Sciences which has involved bilateral visits. Although the focus has been on potatoes for this UN International Year of the Potato, there are collaborations in the field of soft fruit and soil science. Scientists have visited the Institute of Soil Science of the Chinese Academy of Sciences to present their research as part of an MoU and several joint articles have been published.

Research funding from the European Union encourages collaborative projects across Europe. SCRI has had success in applying for these grants; two FP7 projects awarded this year will contribute part of their overall budgets of €16.5m to SCRI. The aim of one is to produce crops with smaller requirements for added nitrogen and the aim of the other is to look at the control of meiosis and its impact on breeding new crop varieties. These add to the portfolio of EU projects in which SCRI is involved. Northern European cooperation in studying sustainable crop protection has been strengthened by MoU with Bioforsk in Norway and Instituut voor Landbouw- en Visserijonderzoek (ILVO) in Belgium. Other less formal partnerships exist at both institutional and individual scientist level, the products of which can be seen by the scientific publications and the visiting workers always to be found in Invergowrie. Scotland shares climatic conditions suitable for berry growing with many Northern European countries and collaboration in all aspects of berry research is ongoing.

The Consultative Group on International Agricultural Research (CGIAR) is an international strategic alliance with the aim of mobilising science for the benefit of the poor. SCRI has close relationships with many of the institutes but has signed MoU with the International Center for Agricultural Research in the Dry Areas (ICARDA) based in Syria and the International Potato Center (CIP) in Peru. The Director General of CIP, Dr Pamela Anderson, addressed SCRI's Improving International Potato Production conference during her visit. CIP and the Commonwealth Potato Collection regularly provide material for breeding new potato varieties. Syria is part of the area where wild barleys are



The Norwegians from Bioforsk enjoy a tractor tour of SCRI. This visit was to celebrate the MoU between the two organisations

found and joint working with ICARDA is very important for SCRI's genomic work on barley.

The most recent MoU is with Michigan State University to develop collaborative programmes in the fields of crop improvement, plant and soil microbial genetics, environmental studies, horticulture and soil carbon sequestration. This and the relationship with the University of Adelaide contribute to a world class axis for genomics.

SCRI is well known for its potato research. EU funding has been won to support the Potato Genome Sequencing Consortium. This Consortium aims to map exactly where different genes responsible for traits like taste, colour, tuber shape and disease resistance reside to enable the breeding of new varieties with desirable characteristics. SCRI along with Dundee University, Imperial College London, and the Agriculture and Food Development Authority (TEAGASC), Ireland are looking at chromosome 4 with other international partners from Argentina, Brazil, Chile, China, India, Netherlands, New Zealand, Poland, Peru, Russia and the United States sequencing other chromosomes. Malawi's special relationship with Scotland has enabled them to get advice and collaboration on growing and exploiting potatoes for the benefit of their people. Visitors to SCRI included Dr Pamela Anderson, the Director General of CIP in Peru, Dr S K Pandey, Director of India's Central Potato Research Institute, and Professor Richard Visser of Wageningen University. These and delegations from Japan, Egypt, Israel, Australia, Ireland, USA, Spain attended Potatoes in Practice.

Review of Events – Highlights

It was a year in which we 'bought the farm'! We saw a Chief Constable examining a 'crime scene' at SCRI...a TV presenter taking her farmer father on a tractor ride... an artist hanging pictures next to laboratories...a senior Scottish politician scanning the shelves in our new information centre and a public health minister eating the fruits of our labours!

A glance at the SCRI 2008 diary explains all. It also gives a clue as to why our organisation remains a centre of research achievement and an important voice in the Scottish debate about climate change and the ways in which we can run a sustainable economy and protect our beautiful surroundings. Closer to home, SCRI remains at the heart of Dundee's life science revolution and strives to be a good neighbour to its local community.

The dawn of 2008 heralded the opening of SCRI's refurbished library and its transition to a fully fledged 'information centre' where much of the hard slog of research is done by e-subscriptions to e-journals. Michael Russell MSP, the Scottish Government's



Environment Minister Michael Russell MSP (right) opens the new Information Centre. Librarian Ursula McKean (left) and Information Services Manager, Sarah Collier (centre)

Environment Minister is himself a man of letters and the co-author of a challenging book on Scotland's future. On a tour of SCRI, he formally opened the centre and met staff involved in its reorganisation.



John and Susan Smith examine plans of Balruddery Farm with the Director.

The new year also saw the completion of lengthy negotiations for SCRI's purchase of Balruddery Farm and the transfer of 118 hectares of prime farmland at Fowlis in the Carse of Gowrie to SCRI ownership. An informal signing ceremony was held involving the owner of Balruddery, John Smith, his wife Susan and the SCRI Chief Executive, Professor Peter Gregory. The farm had been operated by the Smith family for three generations since 1961. (See Page 64 for an article by SCRI's Sustainability Champion, Dr Cathy Hawes, in which she details our plans for the farm that will see it becoming a research facility unique in the UK.)

The future of SCRI is guided by a distinguished board of governors drawn from business and academia. In March we said farewell to Professor Bernard King who stepped down after 10 years on the governing board, with five years as Chairman. Bernard, the Principal and

Vice-Chancellor of the University of Abertay Dundee, was guest of honour at a surprise farewell dinner; a presentation was also made to him at the Institute.



Bidding farewell to Bernard King.

The new Chair of the SCRI Governing Board was announced shortly afterwards. Peter Berry is President of the Crown Agents Foundation, established in 1997 to succeed government as the owner of the Crown Agents for Overseas Governments and Administrations. Mr Berry, who had joined the Board earlier, hails from Fife. The Board was also joined by Mr Sandy Morrison who spent 37 years with Unilever Foods in senior roles in research and development. He spent many years abroad working in Europe, Asia and Africa.

Scientists in the limelight early in the year included Dr Alison Roberts. Alison leads the Cell Biology and Imaging Group at SCRI and was awarded the 2008 Peter Massalski prize. The award ceremony took place at the annual general meeting of the Scottish Society for Crop Research, who administer the prize. It is awarded



Dr Alison Roberts winner of the 2008 Peter Massalski prize..

biennially to the person under 36 years old who is considered to have done the most meritorious research



LEAF Open Farm Sunday at Gilston Mains, Fife

Once again SCRI was represented with a display at Gardening Scotland and the same weekend, a group of scientists underlined our role as a LEAF Innovation Centre by taking part in Open Farm Sunday as the guests of Edward Baxter at his Gilston Mains farm in North East Fife.



Dr Gordon McDougall with eight-year-old Jamie Jones at Open Farm Sunday

One of the undoubted highlights of the year – and representing the greatest, collective outpouring of imagination, ingenuity and sheer hard work – were the SCRI Open Days which took place in June. Friday 6 June was devoted to schools and invited guests; Saturday 7 June was for the general public. Six hundred



The Living Field in full bloom during the SCRI Open Days.

pupils, students and teachers were catered for with a complex timetable of events and activities during the first day. A gloriously sunny Saturday saw 900 people coming through the gates.

Science stuffy? The visitors were treated to the history of whisky, a 'crime scene' constructed by the Plant Detectives, a non-stop cookery marathon laid on by the Tasty Tatties team, a chance to try Barley Bread, DNA extraction, robotics, the Scientists Zoo, bug building, face painting and a chance to get 'hands-on' at the meteorological site.

The foregoing are just a sample of the activities planned, constructed and staffed by SCRI members of staff. In

total there were 10 activity centres on the site and 50 stands, stalls and displays.

Hard on the heels of the Open Days were the Royal Highland Show and SCRI's three specialist events for stakeholders: Cereal Solutions (now renamed Cereals in Practice), Fruit for the Future and Potatoes in Practice. The weather was not entirely kind to the events this year: high winds battered the marquee during our cereals afternoon; rain threatened the soft fruit enthusiasts and almost put paid to Potatoes in Practice!

Seventy visitors made the trip to Gourdie for our briefing on cereals work; another 70 packed SCRI's seminar room to hear the latest in soft fruit research two days



STV's Susan Nicholson – a guest of honour at the Open Day on Saturday 7 June.



Chief Constable of Tayside, John Vine, examines the Open Day "crime scene".

later. And despite highly unusual rainfall statistics in August, we managed a record turnout for the UK's largest potato sector field event, Potatoes in Practice. More than 700 visitors braved the mud to experience the most comprehensive event to date. Once again, many SCRI staffers helped to make the day a success... including the Field and Glasshouse team who managed to build a temporary road to bring traffic safely on and off the site. 2009 will see both Cereals in Practice and Potatoes in Practice move to their new, permanent home at SCRI's Balruddery Farm.



The Improving International Potato Production conference, 8 August.

2008 was the UN International Year of the Potato. SCRI and its commercial arm, Mylnefield Research Services, could not let this pass unmarked in Scotland. So it was that the day after Potatoes in Practice, we staged the Improving International Potato Production conference at Dundee's Apex City Quay Hotel. Eighty-five delegates, including 12 overseas guests, spent a day watching presentations on the latest in potato research and marketing.

The keynote speaker was the Director General of the International Potato Center in Lima, Peru, Dr Pamela



Chinese conference delegates watch the Olympic Games opening ceremony.

Anderson. Fittingly – on the day Beijing stunned the world with the opening ceremony for the Olympic Games, another guest speaker was Ma Shuping, the Deputy Director-General of the Department of Crop Production at the Chinese Ministry of Agriculture.

The conference was the brainchild of a regular visitor to the People's Republic, Dr Nigel Kerby the Managing Director of Mylnefield Research Services. Three potato industry companies and three local authorities and agencies supported the conference.

The previous evening, about 100 guests attended the Branston potato industry dinner organised to tie in with both Potatoes in Practice and the IIPP conference. It was also an opportunity to pay tribute to Jim Godfrey OBE. Jim Godfrey has for many years been a major player in the potato industry, both as a grower and member of the Potato Marketing Board, SCRI and other bodies. He was honoured with a special presentation made by the newly appointed Chairman of the Potato Council Ltd., Allan Stevenson, who is also a member of the SCRI Governing Board.



Jim Godfrey (right) with Potato Council Chairman Allan Stevenson.

The Royal Highland Show started in sunshine and ended in a flood! Once again SCRI events staff and scientists staffed displays in the Royal Highland Education Trust building and the SAC pavilion. Here we constructed a striking display representing a unique site in the Middle East called Evolution Canyon. The canyon is a priceless, long-lived natural evolutionary laboratory. Findings from SCRI's research indicate that there is a tremendous genetic potential locked up in the wild barley collections to be found there.



Public Health Minister, Shona Robison MSP launching (and tasting) the Glen Fyne raspberry.

Soft fruit research and development was recognised during a visit by the Scottish Government's Minister for Public Health, Shona Robison. The Minister met the Director and senior members of staff. She was particularly interested in the work being done on the health benefits of berries. Appropriately Shona kindly officiated in the launch of the latest SCRI/Mylnfield raspberry, Glen Fyne.

For the last two years, SCRI has been the scene of an extraordinary fusion between science and the arts. Ronnie Forbes RSA has been working as the

Much of the research and information SCRI generates is reflected at www.scri.ac.uk

Since its launch in 2007 the SCRI website has attracted more than 100,000 unique visits with users around the world reading about the Institute's work. Throughout the year much effort has been made by staff in the science programmes to ensure their very latest findings are being shared online. Audio and video is now being commissioned to augment the content.



The ARTFEST exhibition at SCRI in October.

Leverhulme Trust artist-in-residence. 2009 will see his work on show around the country. Ronnie's commitment to SCRI was demonstrated by his singlehanded organisation of "Artfest", a month long exhibition of art and craft work by members of staff together with an evening musical concert. Staff were also invited to an open evening at Ronnie's studio in Dundee.

SCRI continued to make the news. There was TV coverage of our project that is aimed at identifying bioactive compounds in blackcurrants thought to be capable of reducing the risk of progression of Alzheimer's disease. The television cameras also recorded Professor David Hopkins' work in Antarctica, the restoration of the Chris North lilies to SCRI and the work underway to map chromosome 4 of the potato as part of the international Potato Genome Sequencing Consortium.



An SCRI appearance on STV's North Tonight.

Successful research outcomes and knowledge exchange events provided a rich source for our publications. A discovery made by scientists at SCRI suggested links between the disease agent that caused the Irish Potato Famine and the tropical scourge of malaria. It resulted in an article in the prestigious journal *Nature* showing that a key sequence of proteins produced by the late blight agent, *Phytophthora infestans*, resembles a recently reported translocation signal in virulence proteins of the malaria parasite. The paper was widely covered in the media.

Dr Vivian Blok and Dr John Jones were among the authors of an article in *Nature Biotechnology* on the



From left: Professors Howard Davies, Simon Gilroy and John Brown. Simon delivered the 2008 Distinguished Lecture in Plant Sciences.

genome sequence of the metazoan plant-parasitic nematode *Meloidogyne incognita* (root-knot nematode). The significance of this work can be appreciated when one considers the annual loss to world agriculture caused by these pests is estimated at \$157 billion.

SCRI's contribution to the Scottish Government's cross-cutting themes of Climate Change, Sustainability and Biodiversity was underlined with the publication of three booklets outlining our work in these areas.

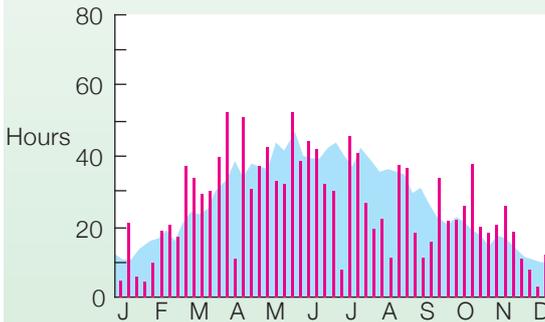
The breadth of expertise assembled for the Improving International Potato Production conference in August enabled SCRI to publish a highlights booklet containing extracts from the presentations made during the day. Another of SCRI's publications, '*101 things you wanted to know about potatoes...but were afraid to ask*' was taken up by the potato supply company, Albert Bartlett & Sons (Airdrie) Limited. They brought in two distinguished chefs, Andrew Fairlie and Michel Roux who added their own potato expertise in an informative, recipe-packed book called *All About Potatoes*.

Among many distinguished visitors to SCRI during the course of the year was Simon Gilroy, Professor of Botany at the University of Wisconsin, Madison in the United States. He gave the 2008 SCRI and College of Life Sciences Distinguished Lecture in Plant Sciences at the University of Dundee. His topic was 'Feeling Green: Mechanical Signaling in *Arabidopsis* Growth and Morphogenesis'.



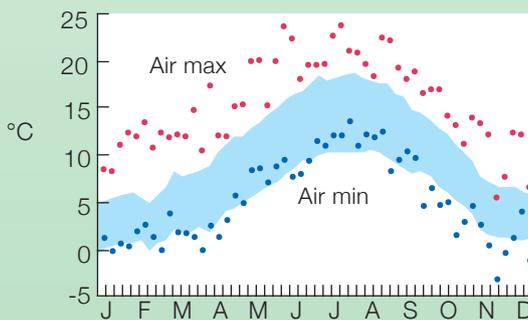
The SCRI website weather pages went live in December 2007. These consist of a general overview page and a data page. The overview page briefly explains the value of meteorological data, the use it is put to by staff within and by bodies or individuals outwith SCRI, and the type of data available. The 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.

Sunshine



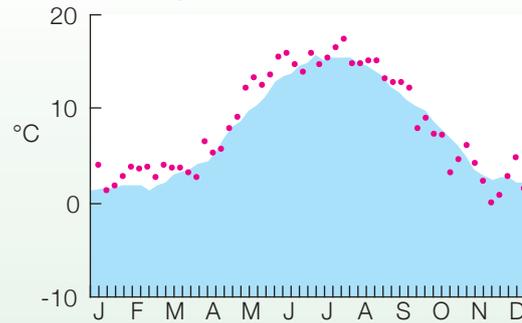
Our observations during 2008 showed average maximum air temperatures equal to or higher than the Long Term Average (LTA), with the exceptions of August at 18.5°C (LTA 18.8°C) and October at 12.2°C (LTA 12.4°C). Most significant were February at 8.9°C (LTA 6.4°C), the highest since 1998; and May at 15.7°C (LTA 13.3°C). Highest maximum air temperatures recorded on individual days reached 20.1°C, 23.7°C, 23.8°C and 22.5°C for May, June, July and August.

Air temperature



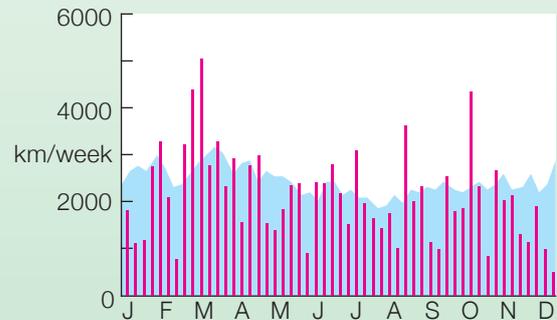
The year is likely to be remembered for its exceptional rainfall. Once again levels were higher than normal, the annual total reaching 781mm as compared to the LTA of 664.5mm. Although only five months had more than normal rainfall, the amounts were significant. January had more than double with 154.3mm (LTA 67.9). It also had 11 days with >5.0mm rainfall, the most on our records for January, with only five other instances of this number in any month, since 1954. Similarly, July had double with 104.5mm (LTA 52.7). August, with 141.5mm had almost three times the expected 52.3mm, 27.7mm falling on the 12th alone. Of the months with less than expected rainfall, May was most notable with 18.7mm against the LTA of 48.0mm.

10cm soil temperature



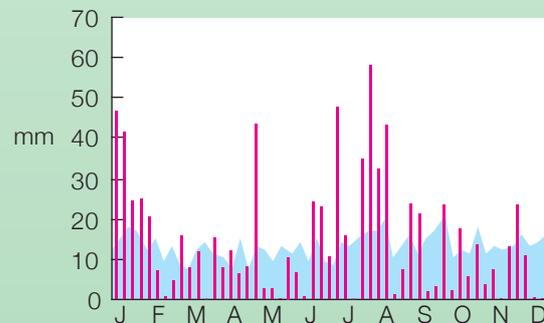
The SCRI Meteorological team has many customers beyond the website. Each month the *Dundee Courier* and *Evening Telegraph* publish a summary of the previous month's weather which is provided by SCRI's meteorological observers.

Run of wind



Average minimum air temperatures showed mixed results with January, February and May to September all boasting higher than typical temperatures, most noteworthy being May with 8.0°C (LTA 6.0°C), while March, April and October to December were all slightly lower than their LTA.

Rainfall



Blue areas on figures indicate long term average 1961–1990

We welcomed several new members of staff during the year. As a way of welcoming them and helping them adapt to their new working life, Human Resources held several Induction Days at which newly arrived staff members were treated to presentations from department heads and a tractor tour of the site.

During the autumn, Human Resources organised an Employee Benefits Awareness Day. Staff were invited to see presentations on pensions benefits, AVC schemes, childcare vouchers and the Cycle to Work Scheme. Information was also provided on the BBSRC Employment Code, SCRI policies and procedures and the counselling service available to all staff.



Receiving the Double Tick award.

SCRI also added a Double Tick award during the course of the year. The disability symbol has been developed so that employers can show their commitment to good practice in employing people with disabilities. It also enables disabled people to know which employers will be positive about their abilities.

During the 12 months we also said farewell to several long-serving members of staff, some of whom had worked at SCRI for more than forty years. They included



Strolling to retirement...leaving us in 2008 were: Bryan Griffiths, Jim McNicol, Stuart Gordon, Bruce Marshall and Alf Low MBE.

Stuart Gordon, Bryan Griffiths, Jim McNicol, Bruce Marshall and Alf Low MBE. Jane Yildz (formerly McNicol) received a long service award.

The organisation maintained its focus on health and safety, quality assurance and environmental management during the course of 2008. We achieved recertification audits of compliance with the management standards EN ISO 9001:2000 (quality assurance), EN ISO 14001:2004 (environmental) and BS OHSAS 18001 (health and safety) during September 2008. Work is underway to achieve UKAS accreditation under the new version of the health and safety standard BS OHSAS 18001:2007 in spring 2009. Audits of SCRI's Business Continuity Plan were carried out by our internal auditors and insurers. Points raised are being actioned and will be incorporated as appropriate into the annual proving exercise of the plan in March 2009.



CEUG Water Workshop.

SCRI's overseas links are recorded elsewhere in the Annual Report. But it has been our pleasure during the course of the year to welcome guests from some of our collaborators and partner organisations. They included the ILVO, Flanders, Michigan State University in the USA and Norway's Bioforsk. The Institute was also proud to host the UK Controlled Environment Users' Group (CEUG) 2008 Water Workshop.

Despite such an action-packed year, SCRI staff still managed time to party. This was because of the work of the SCRI Staff Association which continued during the year to raise funds for good causes, organise quiz nights and ceilidhs, a summer barbecue and many other entertainments and services for members, including retiral presentations. By the end of the year, the funds raised for good causes had reached £1230.



Genetics

Robbie Waugh

Genetics contains around 90 staff, including four fully integrated research groups from the University of Dundee, Division of Plant Sciences. Our work focuses on three groups of crops: potatoes, soft fruits and barley, and incorporates work on model and related species. A dedicated bioinformatics capability underpins our research and we maintain strong interactions with Biomathematics and Statistics Scotland (BioSS – page 57). Genetics manages the Institute Sequencing and Microarray Facility and in 2008 established an Institute Functional Genomics Facility.

This year we welcomed new appointments in barley pathology (Mark Loosely), abiotic stress in potatoes (Ankush Prashar), informatics support for next generation sequencing (Micha Bayer) and developmental genetics in barley (Arnis Druka). We celebrated the joint appointment of John Brown as the head of the Division of Plant Sciences at the University of Dundee and have seen interactions between Genetics and Plant Sciences staff flourish through joint publications and funding. In 2008 we were reviewed twice: once for the RERAD Programme 1 mid term review and once for a rolling series of programme scientific reviews conducted by an international panel of experts. I am pleased to report that we continue to produce measurable outputs in all of our main areas of activity, including PhD-trained staff, software, publications, and new plant cultivars. Some

examples of our research achievements in 2008 are summarised below.

Potatoes are rapidly becoming a staple for the world's poor and now have higher production in the developing world than the developed one. As an estimated six billion people in the world suffer from malnutrition caused by micronutrient deficiency, the micronutrient balance of potatoes has increasing importance. Gavin Ramsay and colleagues have been investigating the genetics of micronutrients in potato tubers in two projects. In the first, natural variation in the levels of tuber carotenoids is being explored through collaboration with Mark Taylor (PPFQ). *crtR-b2*, a gene encoding a β -carotene hydroxylase 2, has been confirmed as the major determinant of high carotenoid



Robbie Waugh

levels in tubers (Fig. 1). Small insertions and deletions in the gene enable the discrimination of alleles on the basis of size which is important for the application of marker assisted selection in crop improvement. Microarray experiments have identified several other genes associated with the trait including transcription factors that may coordinate pathway regulation. In the second, the genetic control of mineral content is under investigation with Philip White (EPI) and colleagues at Nottingham University. Germplasm collections and segregating populations have been explored, and genetic variation for several traits has been found. For example calcium, one of three mineral deficiencies in many diets, varies in a four fold range in a population of plants derived from Andean tetraploid potatoes. Levels of variation for other nutritionally significant



Figure 1 Potato tubers showing different carotenoid contents.

minerals such as iron and zinc suggest that breeding for enhanced levels would be worthwhile.

Ingo Hein, Glenn Bryan and colleagues have identified a collection of 37 bacterial artificial chromosome (BAC) clones from a library made from a diploid potato clone that expresses high levels of quantitative resistance against late blight, and anchored them to the potato genetic map. Full length *Rpi-blb3*-like candidate resistance genes (*R* genes) have been amplified from these BAC clones, from genomic deoxyribonucleic acid (DNA) and complementary DNA (cDNA). With colleagues in the Netherlands, an *Agrobacterium*-based transient expression assay (ATTA) has been developed to functionally test *R* gene candidates in *Nicotiana benthamiana*. Candidate *R* genes are expressed alongside the positive control *Rpi-blb3* (from Dr Edwin van der Vossen) using binary expression vectors. Inoculated sites are subsequently challenged with *Phytophthora infestans* and the outcome compared between the positive control and the candidate genes (Fig. 2). Several genes are currently being cloned into a suitable ATTA vector for this functional analysis.

Along with partners in Ireland (TEAGASC), Imperial College London and the University of Dundee, Glenn Bryan, David Marshall and colleagues aim to



Figure 2 Candidate resistance genes are over-expressed in *Nicotiana benthamiana* via *Agrobacterium tumefaciens* utilising binary vectors (left) alongside a positive control, *Rpi-blb3* that governs an Avr2 specific response. Two days post *Agrobacterium* inoculation, areas expressing the *R* genes are subsequently challenged with *P. infestans*. *Rpi-blb3* mediates resistance towards the *P. infestans* isolate Py23 (top panel) but is ineffective towards *P. infestans* isolate 01/29 (bottom panel).

sequence potato chromosome 4 as a contribution to the International Potato Genome Sequencing Consortium. They are making use of a physical map that is genetically anchored to an Ultra High Density (UHD) genetic map that was constructed previously in 'APOPHYS', a collaborative EC FP6 project. Glenn Bryan along with colleagues from Imperial College, the University of Nottingham, and the Wellcome Trust Sanger Institute, is also involved in sequencing tomato chromosome 4. 19Mb (approximately 85% of the euchromatin) is currently completed. The tomato and potato sequences will be powerful resources for comparative genetics within the Solanaceae and for cross species gap closure in the assembled sequences.

Functional genomics studies in potato have progressed through use of the community Potato Oligo Chip Initiative (POCI) microarray platform. The role of auxin-response genes in the molecular regulation of potato somatic embryogenesis has been investigated and, in collaboration with PPFQ, key expression differences between potato germplasm differing with respect to carotenoid content and other quality traits have been identified. Current work is focused on genetic

and functional analysis of a subset of the identified candidate genes which have been prioritised by knowledge of the relevant biochemical pathways (for example, terpenoid synthases, pectin methylsterases).

Exploring and understanding plant biodiversity in natural and managed agricultural systems is a major challenge. Joint development of two 1536-plex single nucleotide polymorphism (SNP)-based barley genotyping platforms (BOPA1 and BOPA2) with Tim Close in the University of California has enabled quick, cheap and accurate genotypic characterisation of any given barley variety, accession, breeding or mutant line. Using this platform Joanne Russell, Luke Ramsay, Jordi Comadran, Andy Flavell (University of Dundee) and others have focused on clarifying the relationships between different barley populations and investigating the link between sequence variation, recombination and linkage disequilibrium. They have assembled extensive collections of barley germplasm including cultivars, globally distributed landraces and wild progenitor collections. Using BOPA1 and 2, they have demonstrated that whole genome association scans can be successfully applied to locate the genes

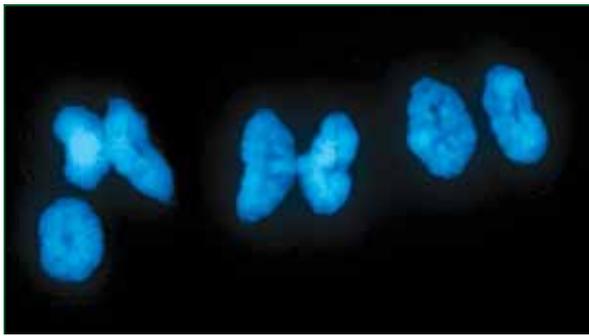


Figure 3 Barley chromosomes at meiosis.
(Courtesy of Dr. Sue Armstrong, University of Birmingham).

controlling a range of phenotypes. These studies have highlighted a severe lack of recombination in the barley genetic centromeres, which contain 30–50% of all barley genes. Consequently, these areas appear almost immune to crossing over during meiosis, impacting upon the release of genetic variation in breeding (Fig. 3). These observations have led to a significant, BBSRC-

funded collaboration between Luke Ramsay, Claire Halpin (University of Dundee) Sue Armstrong and Chris Franklin (University of Birmingham) and Glyn Jenkins (University of Wales, Aberystwyth).

Arnis Druka also used the BOPA platform to characterise a unique population of plants known as the ‘Bowman collection’. The collection was developed by Jerry Franckowiak at the University of North Dakota by repeated crossing followed by phenotypic selection of 977 mutant lines to the same recurrent parent – the cultivar Bowman – effectively generating a set of Nearly Isogenic Lines. These 977 lines represent the majority of the characterised morphological and developmental variation described in barley over the past 80 years. A comparison between Bowman and each individual ‘Bowman line’ identified polymorphic markers encompassing the mutant gene that could be

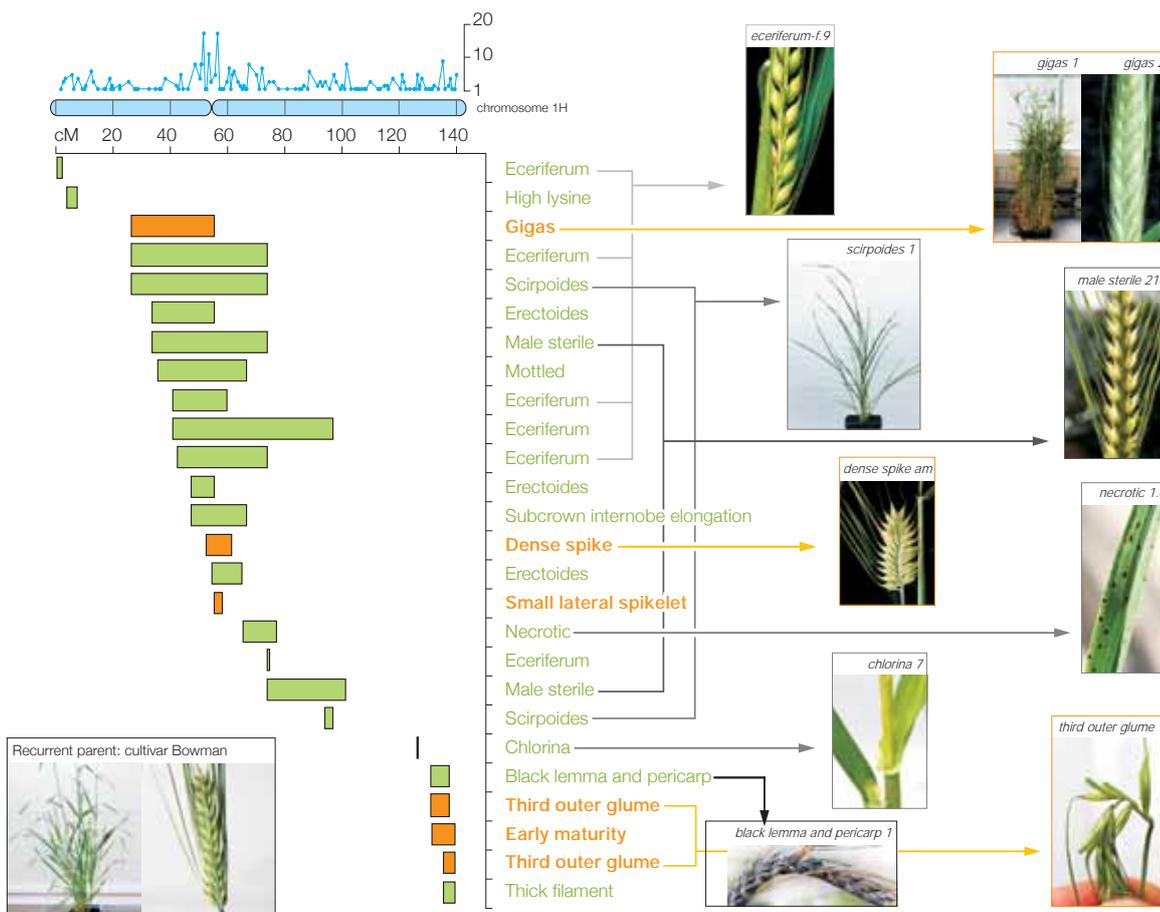


Figure 4 Twenty-six Bowman lines were selected based on polymorphisms located on barley chromosome 1H. The bars on the graph represent the genetic interval containing mutant alleles. The mutant names are highlighted in orange or green text to the right of the graph. Our targets for cloning are highlighted in orange and images of selected phenotypic variants are shown.

arranged according to their genetic map location. This exercise addressed a number of important objectives: it defined the location of the mutated genes, it assessed their distribution in relation to the gene-based SNP marker map and it identified how successful increasing rounds of backcrossing had been in eliminating donor genomes.

Quantitative trait locus (QTL) analysis of malting quality has been practiced widely, but has generally revealed different locations for the contributing genetic factors. While this has often been attributed to differences in the germplasm studied, effects of growing and processing environments are also important. Growing conditions can promote a friable grain structure, give greater likelihood of dormancy or reduced enzyme production. Similarly, processing regimes are determined by end user specifications and may emphasise different attributes of the barley grain. Stuart Swanston and Bill Thomas conducted QTL analysis on data from a population derived from a cross between the German variety Triumph and the US variety Morex grown in Scotland, Spain and the USA. QTL were distributed across all seven chromosomes. However, positive alleles for quality were observed in both parents and consistent effects were correlated with the position of genes known to be involved in cell wall biosynthesis and grain structure. Some of the progeny performed better than the original parents for several traits illustrating the potential of bringing together positive alleles from each germplasm source.

Barley leaf rust caused by *Puccinia hordei* Otth. is one of the model systems to investigate basal resistance that is inherited in a quantitative manner. In collaboration with Rients Niks in the Netherlands, Xinwei Chen has explored the molecular basis of quantitative resistance to leaf rust in the Steptoe x Morex reference population through an integrated strategy combining microarray based time course experiments, genetical genomics and genetic mapping. After collecting expression data from all lines in the population 18 hours post infection, correlation analysis between gene expression and rust resistance has revealed 128 genes significantly correlated with resistance. The most highly correlated 24 genes exclusively mapped to *Rphq1*

which had the largest effect on the phenotype. These candidates are currently under further investigation.

Resistance to some fungal diseases in raspberry is associated with morphological characters, particularly cane pubescence (Fig. 5), an epidermal cell trait determined by gene H (HH or Hh giving hairy, hh giving hairless canes). Julie Graham, Mary Woodhead and colleagues have mapped gene H to *Rubus* linkage group 2 (LG2), closely associated with resistance to cane botrytis and spur blight. Gene H is also associated with QTLs for cane spininess, and fruit ripening where development from open flowers to green/red fruit is delayed by up to two days in Hh genotypes compared to hh genotypes. Their challenge now is to identify the genes in this region and determine how they contribute to these traits. BAC libraries previously constructed from the resistant parent will be invaluable in this endeavour.

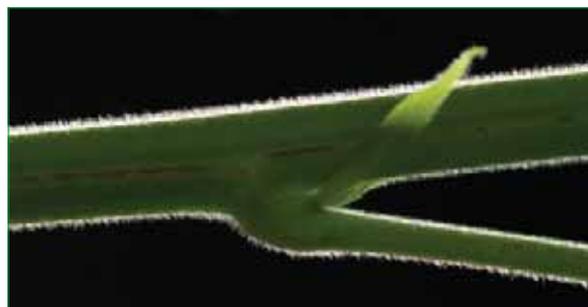


Figure 5 Hairy raspberry cane.

In collaboration with The World Agroforestry Centre with funding from Rothamsted International African Fellows Programme, Joanne Russell has assessed the level and distribution of genetic variation in the indigenous African fruit tree *Allanblackia* (Fig. 6), the subject of increased interest for edible oil production for the global food market. Until recently *Allanblackia* has been largely an overlooked wild tree and very little was known about the biology of the genus to guide conservation and use in the transition from wild harvest to cultivated production. We assessed the genetic composition of populations of five *Allanblackia* species. Data indicated significant differentiation between some taxa. Genetic relatedness between species and geographic proximity sometimes – but not always – corresponded, an observation that likely reflected complex evolutionary processes related



Figure 6 *Allanblackia*

to migration and dispersal in the genus. Our data suggest that Cameroon presents particular challenges for conservation and opportunities for domestication of the genus.

Gene expression is regulated by networks of transcriptional control and further modulated by post-transcriptional processes. One of these, alternative splicing (AS), is an extremely important, but understudied, mechanism affecting at least a third of plant genes. AS is involved in plant development, signalling and response to biotic and abiotic stresses. It generates proteins with different domains which can affect their localisation, activity and ability to interact with other proteins or substrates. John Brown, Craig Simpson and colleagues have developed a system for analysing multiple (>300) plant AS events simultaneously and are using this system to address how AS is regulated in general, its role in controlling expression in specific pathways and processes and how AS and gene expression are influenced by external stimuli such as temperature. They have shown that proteins that bind to the 5' ends of messenger ribonucleic acids (mRNAs) can affect AS of the first intron and that SR protein splicing factors regulate AS of sets of different transcripts. Approximately 15% of AS transcripts are targeted for degradation and thereby regulate gene transcript levels and alternative splicing. Their multiplex AS assay has rapidly become the foundation for numerous interactions with labs across Europe.

Post-transcriptional processing of mRNAs occurs in the nucleus of the cell (Fig. 7). The nucleolus is the

major sub-compartment of the nucleus and is now recognised to have multiple functions in processing of diverse RNAs and assembly of RNA-protein complexes. After finding mRNA-associated proteins in the plant nucleolus John Brown and Craig Simpson have recently and unexpectedly discovered mRNAs in the nucleolus. Moreover, the nucleolar mRNAs appear to be enriched for improperly processed variants that are detected by an mRNA quality control mechanism and destroyed. This link between the nucleolus, aberrant mRNA processing and mRNA quality control is unique to plants and demonstrates a new function for the nucleolus.

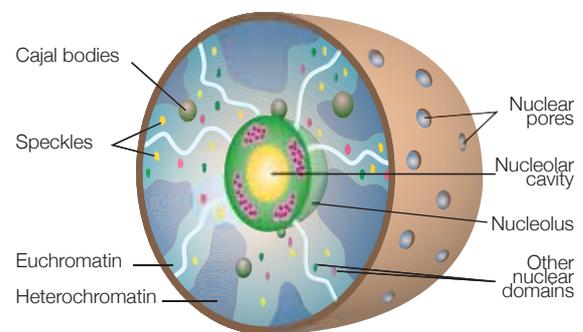


Figure 7 The plant cell nucleus.

Ian Milne and David Marshall have led the development of 'Flapjack', a new visualisation tool that facilitates the analysis of data generated by high throughput SNP genotyping technologies (Fig. 8). Its graphical displays are rendered in real time allowing for rapid navigation and comparisons between lines, markers and chromosomes. Flapjack provides a number of graphical

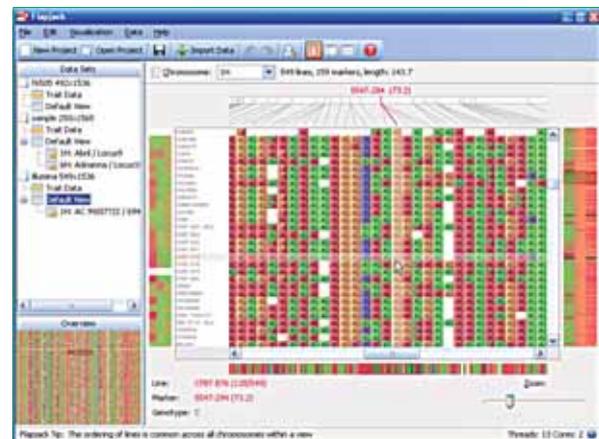


Figure 8 Screenshot of 'Flapjack' graphical genotyping and analysis software.

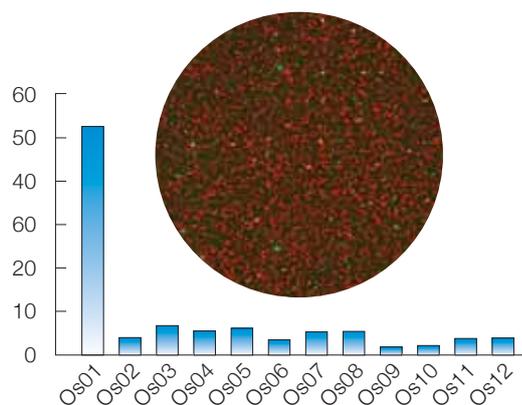


Figure 9 Barley array probed with reference barley RNA (red), which allows spot identification, and a single pool of approximately 400 BACs derived from chromosome 3B of wheat (green). Green/orange spots identify homologous genes within the BAC pool. Success of the approach is confirmed by comparison of positive probe sequences with rice orthologues, where over 50% correspond to rice chromosome 1, which exhibits high synteny with wheat chromosome 3B.

genotype views with individual alleles coloured by state, frequency or similarity to a given standard line. It supports a range of interactions with the data, including moving lines or markers around the display, inserting or deleting data, and sorting or clustering lines by either genotype similarity to other lines, or by trait scores. Any map based information such as QTL positions can be aligned against the displayed graphical genotypes to identify associated haplotypes.

Micha Bayer and Ian Milne have developed OPTIRas, a modular, web based decision support system to assist starch potato growers in the Netherlands and Northern Germany. The system presents both financial and scientific overviews of various scenarios that encompass different combinations of potato cultivars, nematode infestation levels in fields, seed rates, fertiliser regimes, and storage losses after harvest. The system has been developed for use in an internet environment, with all farmer-side interaction being performed via a web browser. Designed to be modular and extensible, the separate components share a common look and feel and are presented to the end user as part of a single, inclusive website.

The Sequencing and Microarray Facility led by Pete Hedley supports genetics based research across the Institute by providing access to state of the art genomics technologies and expertise. In 2008 we installed a BeadXpress (Illumina) platform which processes 96- or 384-plex SNP detection assays and increases genetic marker throughput while minimising costs per datapoint. We have also begun to exploit next generation sequencing technologies through links with UK university service providers. Microarray analysis continues to be used by many groups across the Institute. Highlights include the dissection of flavour and texture components in potato tubers in collaboration with PPFQ and, in a novel approach, the development of an approach that provides high-throughput anchoring of physical and genetic maps (Fig. 9).

Our research in potatoes and soft fruits feeds into downstream breeding programmes managed by SCRI/MRS. The soft fruit programme, led by Rex Brennan and Nikki Jennings, has consistently delivered commercially successful cultivars that dominate their respective industries both within the UK and worldwide. Emerging priorities for soft fruit breeding include the environmental resilience of germplasm, particularly with respect to winter chilling requirements linked to climate change, and identification of genotypes with enhanced health benefits and elevated antioxidant activities from the fruit.

Finally, in 2008, Vales Sovereign, a potato variety bred for Greenvale AP recently won the Tesco Fresh Produce Variety of the Year award, covering all fruit and vegetables. Vales Sovereign was national listed in 2003 and came from a research programme to source parental material having multiple copies of the H1 gene for resistance to the 'golden' potato cyst nematode. It also has excellent resistance to blackleg, blackdot and common scab. It is described as an outstanding 'all rounder'. The nationwide launch by Greenvale AP follows successful commercial trials, where it performed very well in taste panels and sold strongly in test stores.



Plant Pathology

Lesley Torrance

Research in the Plant Pathology programme is focused on economically important diseases and pests of potato, barley and berry fruit. Our research extends from studies on pathogen genes and disease processes at the level of molecules and cells to the epidemiology and evolution of pathogen populations infecting field crops. The knowledge gained is used to underpin sustainable disease control methods by aiding the development of resistant plants and integrated management strategies.

Changes in environmental conditions, for example, changing temperatures, rainfall and CO₂ levels, may influence the incidence and severity of existing pests and diseases or bring new threats to Scottish crops. We have re-focused some of our efforts to investigate this. To this end a major new grant has been secured from RERAD by Dr Ian Toth and colleagues to study the potential threat to Scottish seed potatoes from the bacterium *Dickeya dianthicola* which infects potatoes in the warmer conditions of Southern Europe.

This year, research on the barley pathogen *Rhynchosporium secalis* has been strengthened by the appointment in Plant Pathology of Dr Anna Avrova to study pathogenicity effectors and Dr Mark Looseley in the Genetics programme to study barley resistance genes. Their research will be integrated with the ongoing epidemiology work with the major

aim of developing durable resistance to one of the most destructive pathogens of barley. Bioinformatics research has also been strengthened with the appointment of Peter Cock.

Globodera pallida genomics (John Jones & Vivian Blok)
The sequencing project for *Globodera pallida* is now in progress. This is a joint project between SCRI, Rothamsted Research, The Wellcome Trust Sanger Institute and Leeds University. Genomic libraries have been produced and sequencing from these libraries is underway. Over the next few months a draft sequence will be completed along with extensive RNA sequencing using the Solexa Illumina platform. This transcriptome analysis will assist gene finding and annotation as well as providing quantitative information on the genes expressed in each life stage. We are also using a range of techniques to analyse the function of important

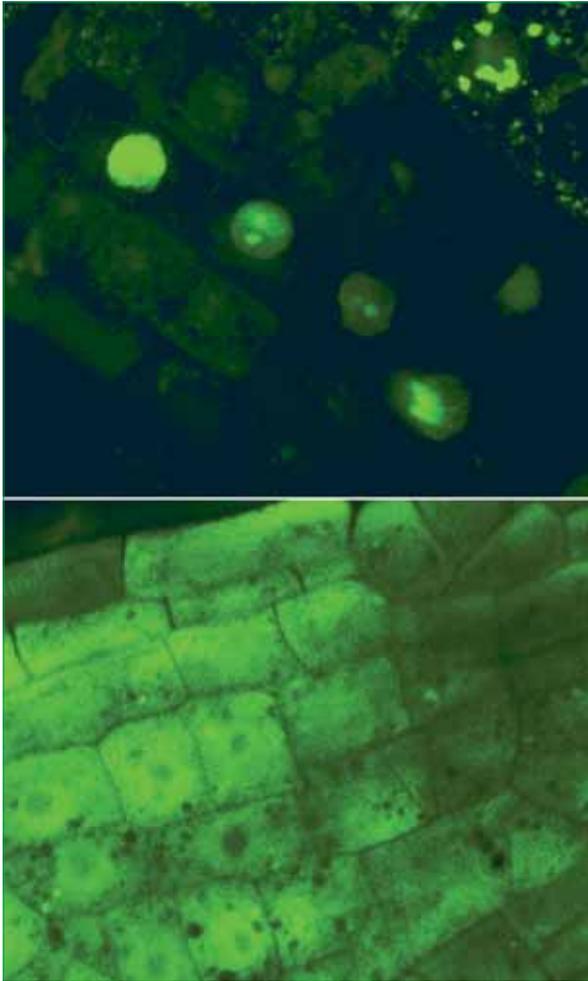


Figure 1 Different members of a family of nematode secreted proteins (SPRYSECs) localise to the nucleus/nucleolus (upper panel) or the cytoplasm (lower panel).

nematode secreted proteins that may play important roles in the plant–nematode interaction. In collaboration with colleagues at the French National Institute for Agricultural Research (INRA) Rennes we have identified a very large family of novel proteins (SPRYSECs) from *G. pallida*. We have examined the subcellular localisation of several members of this gene family and have found that while some remain in the cytoplasm others are targeted to the nucleus (Fig. 1).

Programmed cell death and its role in plant defence

(Michael Taliansky) Animals and plants exploit programmed cell death (PCD) as a means to eliminate redundant and damaged cells during their development and in response to various stresses. Although representatives of both kingdoms share several morphological features of PCD, plants lack

homologues of caspases – a family of highly specific cysteine-dependent proteases that are critically involved in animal PCD. In collaboration with the Moscow State University team (Professor Andrey Vartapetian) we have identified and characterised a subtilisin-like plant protease (SLPP) that, being structurally distinct from animal caspases, appears to be a functional caspase analogue. In contrast to classical caspases which are Cys-dependent proteases, subtilisin-like proteases are serine-dependent (Ser-dependent). Using mutational analysis we have confirmed that SLPP is a real subtilisin-like protease. We next addressed a role of SLPP in plant cell death and development. For this purpose we constructed transgenic *Nicotiana tabacum* Samsun NN plants either over-expressing tobacco SLPP or possessing a markedly decreased level of SLPP activity due to RNA interference (RNAi). Using these transgenic plants we have shown that the newly identified enzyme is essential for PCD activation in response to biotic (*Tobacco mosaic virus*) or abiotic (NaCl and methyl viologen) stresses.

To learn whether homologous enzymes that are responsible for this activity exist in other plant species/crops, we have now purified SLPP activities from potato and barley. Variable amounts of activity have been detected in different *Solanum tuberosum* isolates but only low levels of activity were detected in two *Solanum tuberosum* group *phureja* isolates. Variable amounts of SLPP activity were also detected in different barley cultivars with a transient elevation in activity being observed in plants treated with defence elicitors and infected with *Rhynchosporium secalis*. SLPP activity thus seems to play a role in the defence mechanism of plants against pathogen infection. This also applies to infection of plants with *Agrobacterium tumefaciens* where the agrobacteria VirD2 protein is a substrate for SLPP activity. Mutation of the VirD2 protein to remove SLPP cleavage sites improves the efficiency of gene transfer into a wide range of plant species by agrobacteria, a finding that has commercial significance.

Potato mop-top virus long distance movement

(Lesley Torrance & Eugene Savenkov) Previously it was shown that *Potato mop-top virus* (PMTV) does not infect all parts of the potato plant and that plants grown



Lesley Torrance

from infected tubers can 'escape' infection. This work was based mainly on the detection of the virus capsid protein. The PMTV genome encodes replicase, movement and capsid proteins on three different RNA molecules (RNA-R, RNA-M and RNA-CP respectively). Studies on the movement and systemic spread of the different PMTV RNAs have found that RNA-R and RNA-M can move to upper leaves independently of RNA-CP. More detailed studies of mutant RNA-CP infectious clones showed that systemic movement of RNA-CP is regulated by the capsid proteins but the movement of the other two RNAs is unaffected. It is most probable that RNA-CP free infections are 'dead ends' since RNA-CP is required for virion formation and vector transmission to new hosts. However, our results help to explain the earlier observations of uneven virus distribution and it is possible that the potato plants thought to have 'escaped' infection were actually carrying RNA-R and RNA-M.

[iLOV, a new tool to study cellular processes](#)

(Sean Chapman & Alison Roberts) Green fluorescent

protein (GFP) and similar proteins have been used widely to study protein localisations and dynamics in living cells, and as reporters of virus infection and spread. However, currently used GFP-like proteins are large which limits their use. For instance, viruses expressing FP markers often move poorly between cells and fail to move systemically through plants. In addition, fusion of large FPs to proteins of interest can disrupt their function. In collaboration with Dr John Christie (Glasgow University) and Dr Karl Oparka (Edinburgh University) we have engineered a smaller (~10 kDa) alternative to GFP (~27 kDa) based on a flavin-binding motif derived from the light, oxygen, or voltage-sensing (LOV) domain of the plant blue-light receptor, phototropin. The procedure of DNA shuffling (molecular evolution) was combined with high-throughput, *Tobacco mosaic virus*-based screening to identify LOV derivatives with improved protein stability, optimised *in planta* fluorescence, decreased susceptibility to photo-bleaching and reduced bleaching recovery times. The resulting small molecule, termed iLOV, functions well as a genetically-encoded fluorescent reporter to track



fusion protein trafficking, and can be effectively targeted to label cellular structures such as the nucleus and Golgi apparatus in plant cells. The small size of the iLOV gene improves retention of the reporter gene by viruses and disrupts viral infection processes less. iLOV was expressed either as a free protein or as a fusion to a viral protein from both *Tobacco mosaic virus* and *Potato mop-top virus* and functioned as a superior reporter to GFP, allowing more natural cell-cell movement rates and systemic infections for both viruses. Further expression studies confirmed that iLOV also functions well as a fluorescent marker in animal and bacterial cells.

Phytophthora effectors (Steve Whisson & Paul Birch)

Pathogen effector proteins play a key role in establishing infection and as such are often 'sensed' by the plant as a signal of invasion by a pathogen, triggering defence responses. There is currently an international focus on the effector proteins of *P. infestans* and other oomycete plant pathogens, to understand how effectors are translocated inside host cells, what host plant proteins or processes are being targeted, and which effectors act as avirulence proteins to trigger resistance in diverse host germplasm. We have shown that the RXLR-EER translocation motif is functionally interchangeable with the RXLXE/D/Q translocation motif from the virulence proteins from malaria parasites. Similarly, the RXLR or RXLR-EER motifs from avirulence proteins from the *Arabidopsis* downy mildew pathogen are functionally interchangeable with the translocation motifs from *P. infestans* Avr3a. This suggests that there may either be an ancient conserved mechanism for translocation of effectors inside host cells, or an evolutionary convergent solution from different groups of pathogens to this common problem.

The effector protein Avr3a was used to screen a yeast two-hybrid library of potato genes to identify interaction proteins that may represent the virulence target(s) of Avr3a. This revealed that Avr3a interacts with the potato CMPG1 protein, a ubiquitin E3 ligase. In this system, Avr3a functions as an E2 ubiquitin conjugating enzyme. Ubiquitination is a signalling process found in all cells, and reprogramming or inhibiting it can drastically alter cell fate.



Dr Alison Roberts, Cell Biology and Imaging.

Using a positional cloning strategy, the *Avr2* avirulence gene, matching the *R2* resistance gene in potato, was isolated from *P. infestans*. It also contains the dual RXLR-EER motifs. Interestingly, it is able to trigger a resistance response mediated by *R2*-like resistance genes in a broad range of *Solanum* species.

Monitoring the late blight pathogen (David Cooke & Alison Lees)

Marked changes in the populations of the late blight pathogen *P. infestans* have been recorded over the past two seasons in a Potato Council funded survey of GB potato crops. Over the 2006, 2007 and 2008 seasons we have tested the mating type of over 3500 *P. infestans* isolates from almost 700 late blight outbreaks. On average, the A2 mating type was found in 74% of outbreaks with both mating types found together in almost 20% of outbreaks. The risks of sexual oospore formation are thus high. Such oospores may act as an additional source of primary inoculum and generate a more diverse and adaptable pathogen population. The threats of this dramatic shift have been investigated further by genetic fingerprinting using Simple Sequence Repeat (SSR) markers. We have shown that the population is made up of relatively few clonal lineages and is dominated by a single lineage of the A2 mating type known as genotype 13_A2. This single clone comprised over 70% of the pathogen populations sampled in 2007. Aggressiveness tests using a range of *P. infestans* genotypes against five commonly grown potato cultivars demonstrated that genotype 13_A2 is particularly aggressive, especially at lower temperatures. These results and their implications have been widely reported to the industry.

To further understand the impact of this new pathogen population on disease management and inform future breeding plans we have also re-evaluated the resistance ratings of a range of commercial cultivars and breeding material. As lead researchers in the Eucablight project (www.eucablight.org) we have also been responsible for coordinating the inclusion of information into a database of European isolate data. In 2007 the database was extended to allow the collection of *P. infestans* data from Central and South American countries.

Assays for soil borne pathogens (Alison Lees & Vivian Blok) Soil borne potato tuber blemish diseases including black dot (*Colletotrichum coccodes*), *Rhizoctonia solani* and powdery scab (*Spongospora subterranea*) affect the quality of seed and ware crops in the UK and worldwide. We have improved DNA extraction methods and sampling strategies so that a molecular test (based on real time PCR) can be used for the rapid and accurate quantification of potato pathogen DNA in plants, tubers and soils. Diagnostic tests are used to understand the relative importance of different sources of inoculum and the environmental factors influencing infection and disease development, with the aim of developing effective control strategies. In collaboration with SAC Aberdeen, commercial diagnostic tests along with the information needed to interpret the results and implement integrated control strategies have been delivered to growers.

The new EU PCN (potato cyst nematode) directive which comes into force in 2010 will require many more soil samples to be processed than before. Statutory testing is conducted by SASA – Science & Advice for Scottish Agriculture and is based on microscopic examination of samples which is labour intensive and not suited to processing very large numbers. Therefore, we jointly developed a quantitative molecular diagnostic to assay soil samples for PCN as an alternative. Excellent agreement in terms of sensitivity and accuracy

was obtained in comparative tests and the assay is currently being adapted to a robotic platform for the high throughput of samples.

Enterobacteria in the environment (Nicola Holden & Ian Toth) The Enterobacteria are a large family of bacteria that can persist in many environments and are found in association with hosts from every biological kingdom. The outcomes of their interactions vary from beneficial through to commensal or pathogenic and include many devastating human, animal and plant diseases. Our research centres on bacteria–host interactions that occur naturally in the environment. We have shown that human pathogenic enterobacteria are able to colonise leafy vegetables and arable crops without causing obvious disease symptoms. We have also found plant pathogens that normally cause disease on potatoes are able to colonise other plants in an asymptomatic manner. This shows that differences in the host species can result in different outcomes from the bacterial infection. The recent increase in genomic information has led to a better understanding of these bacteria and has opened the way for research on hitherto unknown aspects of their lifestyle. Research is ongoing into the mechanisms of adherence during the early stages of plant colonisation by both human pathogenic and plant pathogenic enterobacteria. The objective is to identify adherence factors that are required for specific bacteria–host cell interactions. Further work on both groups of bacteria aims to understand the regulatory processes during different stages of infection. This area has progressed considerably over recent time for plant pathogenic enterobacteria and has revealed a complex network that is sensitive to the particular stage of infection as well as a number of environmental cues. The area is at an early stage for human pathogenic enterobacteria. An overarching goal that draws all aspects of the work together is to find the parallels between both groups of bacteria that facilitate colonisation of plants.



Plant Products and Food Quality

Derek Stewart

The programme's research targets have come into sharp focus this year with food now high on the agenda of the public, industry and governments worldwide. Furthermore the tide of consumer education continues apace with the result that the perception of, and demand for, food quality goes well beyond standard organoleptic criteria with impact on human health now a driving factor in many food sectors.

As part of our programme of research we are addressing all of these factors and extending into significant new areas with plant-derived bioactives a particular focus. To this end we have continued to provide evidence for bioactivities and potential health benefits of berry components. For example, polyphenols from a range of berries and fruits were found to inhibit the growth of cultured colon cancer cells with raspberry and strawberry amongst the most effective. This extended our understanding of the most active components and the mechanisms underlying these effects on cancer cells are being further examined through the continuing joint PhD studentship with the University of Ulster. Furthermore this is being expanded at the cancerogenesis level through collaboration with the Biomedical Research Centre, University of

Dundee, and has shown that specific fruit polyphenolics positively influence the expression and translation of key chemoprotective genes such as *NAD(P)H:quinone oxidoreductase 1 (NQO1)* and *Nuclear factor-erythroid 2 p45-related factor 2 (Nrf2)*, which mediates and regulates the transcriptional activation of many genes which encode detoxification and antioxidant proteins in response to redox stress (Fig. 1).

Previous studies suggested that berry components could inhibit key enzymes in the human digestion of starch and thus have the potential to modulate starch digestion thereby influencing blood glucose levels after meals. This could be of benefit to people suffering from, or at risk of developing, type II diabetes. This idea is currently being investigated in a human intervention trial



Derek Stewart

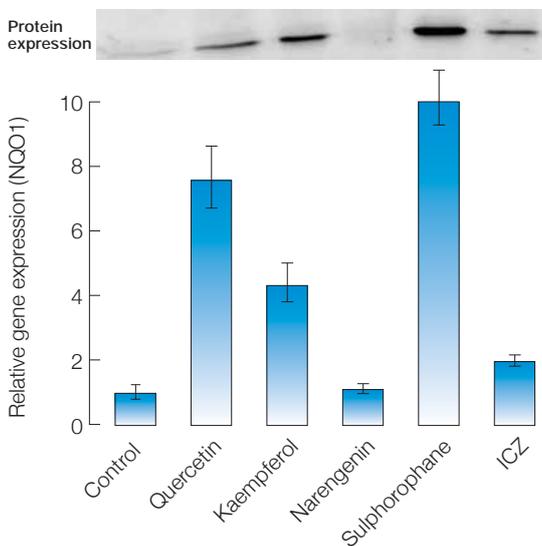


Figure 1 The protein and gene expression levels of NAD(P)H:quinone oxidoreductase (NQO1) in the model systems rat liver epithelial (RL34) cells following treatment with putative dietary anticancer components. Quercetin, Kaempferol and Narengenin and common dietary plant polyphenols, Sulphorophane and ICZ (indolo[3,2-*b*]carbazole) are degradation and digestion products derived from isothiocyanates present in dietary *Brassica* species: well reported sources of anticancer benefits.

with scientists at Queen Margaret University, Edinburgh. We have also confirmed that berry polyphenols can inhibit pancreatic lipase, the key enzyme in the digestion of fats, which could have implications for the control of calorie intake from fatty foods and weight control.

The bioefficacy of selected plant polyphenols has been established with respect to the activation of FOXO transcription factors, the 'master regulators' of cell survival, cell cycle and glucose homeostasis, in cultured pancreatic cells, and has suggested that plant polyphenols such as theaflavins, theaflavin 3-*O*-gallate, theaflavin 3'-*O*-gallate, theaflavin 3,3'-*di-O*-gallate and thearubigins could mimic insulin and potentially influence diabetic processes. This is being explored further via a joint PhD studentship with Dr Graham Rena at the University of Dundee.

The focus on food functionality has been carried through to several EU projects. Within DEVELONUTRI, a project focused on nutritive losses throughout the potato, tomato and wheat processing and food chains, extensive and detailed studies into (anti)nutrient and micronutrient stability have been performed and these are informing the more detailed analyses with respect to sources of quantitative variability. In tandem with

this, extensive ring testing is under way to compare and contrast the standard analytical approaches of Gas Chromatography (GC), Liquid Chromatography – Refractive index (LC-RI), Liquid Chromatography – Ultra Violet (LC-UV) and Liquid Chromatography – PhotoDiode Array (LC-PDA) with the more routine metabolite profiling approaches offered by Gas Chromatography – Time of Flight – Mass Spectrometry (GC-ToF-MS) and Liquid Chromatography – Mass Spectrometry (LC-MS). This is with a view to revising how food compositional database reporting is undertaken and the extent to which these approaches can be developed.

Research in BarleyBread, another EU project, is also addressing the food functionality issues by studying to what extent we can supplant wheat with barley in breadmaking. Barley contains a complex polysaccharide, β -glucan, which, when present in foods at certain levels, has been shown to reduce cholesterol and the likelihood of cardiovascular disease. Indeed β -glucan is one of the few plant-derived components to be given an approved health claim (see inset). Within the project, and in collaboration with the SCRI Genetics programme, we are establishing the biodiversity of β -glucan and other putative healthy components such as sterols, specific polyphenols etc., in a broad range of barley germplasm across Europe with the aim of identifying the national/regional optimal varieties for these health components. Data will inform the use of specific barley germplasm for developing 'healthier breads' for each participating nation.

Furthermore in collaboration with the local food ingredients company, Macphie of Inverbervie, bread with a 20% barley content was produced which performed texturally in a manner analogous to the equivalent 100% wheat bread. Consumer preference testing at the SCRI Open Day in 2008 was a resounding success with



Figure 2 Consumer preference testing at the SCRI 2008 Open Day of bread containing 20% wholegrain barley flour.

>80% of the public preferring the barley bread over the traditional wheat based product (Fig. 2).

With regard to the EU priority area of 'safer and environmentally friendly production methods and healthier foodstuffs' SCRI has played a key co-ordination role in

the EU Integrated Project 'SAFE FOODS – Promoting Food Safety through a New Integrated Risk Analysis Approach for Foods' (www.safefoods.nl). This project has been at the forefront of assessing the potential value of advanced, broad scale analytical 'omics' technologies within a risk assessment framework, particularly with regard to crop breeding and production systems. Using potato and maize as model crop species the project has revealed that variation in gene protein and metabolite expression is large with respect to genotype, growing site and season and even crop management practices. Any differences between GM and non-GM crops tested

were dwarfed by comparison. These approaches could therefore be used to benchmark any measured differences in a particular crop against the extent of 'acceptable' variation within the framework of a history of safe use of the crop species in question. A scheme for the approach is presented (Fig. 3).

The Food and Drug Administration claim (USA) Generic health claim – The inclusion of oats as part of a diet low in saturated fat and a healthy lifestyle can help reduce blood cholesterol

Diets low in saturated fat and cholesterol that include 3 grams of β -glucan soluble fiber from barley (or oats) may reduce the risk of heart disease. The product must contain at least 0.75g of β -glucan per serving. This value is based on the observation that foods providing at least 3g of β -glucan per day are effective in lowering serum cholesterol levels. Spreading these 3g over three daily meals and one snack, they arrived at the figure of 0.75g per serving.

Distribution of Gene Ontology molecular function aThe FDA stipulations on barley β -glucan derived health claims with respect to reduced cholesterol and a reduced risk of cardiovascular disease.

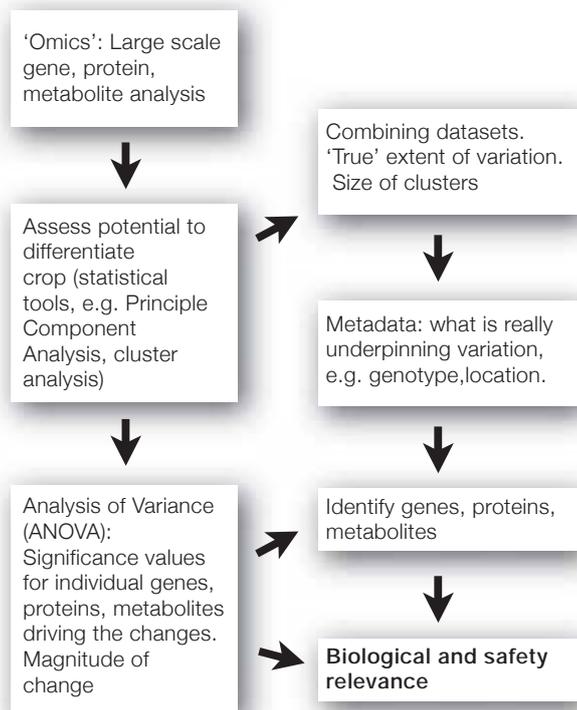


Figure 3 Flow diagram: data-rich outputs of 'omics' feeding into comparative safety assessment.

Potato quality is assuming a greater importance in breeding programmes, with consumers demanding greater variety and retailers wishing to market cultivars that have distinctive commercial advantages. However, as with many food crops, potato flavour is difficult to assess in breeding programmes. Assessments can be highly subjective and require trained sensory panels. Generally these sensory approaches have a low sample throughput and are consequently expensive. As a result, flavour is generally only assessed in the later stages of a breeding programme after selection for essential agronomic qualities and more easily quantifiable traits and as a result most of the potential flavour improvements are likely to be discarded.

Previous studies using trained taste panels have clearly identified the *Solanum tuberosum* Group Phureja (commonly referred to as *Solanum phureja*) type potatoes as having a distinctive and generally preferred flavour compared with Group Tuberosum types (Commonly referred to as *Solanum tuberosum*). Our research has identified candidate compounds that may account for these differences. These include volatile compounds such as the esters of branched

chain amino acids and the sesquiterpene α -copaene as well as umami taste compounds, such as glutamic acid and 5' ribonucleotides. In fact, the levels of the major umami compounds (glutamate and 5' ribonucleotides) in boiled potato cultivars, previously assessed for sensory quality, were significantly higher in two *Solanum phureja* cultivars when compared with two *Solanum tuberosum* cultivars. The equivalent umami concentration was calculated for five cultivars and there was a strong positive correlation with acceptability score from a trained evaluation panel suggesting that umami is an important component of potato flavour (Fig. 4).

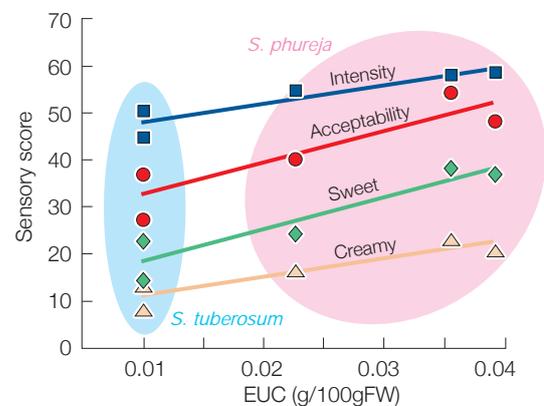


Figure 4 *S. tuberosum* cultivars Maris Piper (MP) and Record were compared with *S. phureja* clones DB333-16 and DB257-28, and cultivar Mayan Gold (MG). Square=flavour intensity; circle=acceptability; diamond=flavour sweet; triangle=flavour creamy.

Potato tuber texture is also a key quality determinant of cooked potato and a major trait that influences consumer preference. As with flavour, texture is a complex trait to analyse as it depends on the interaction of many factors and defining texture that is attractive to consumers also depends on sensory panel analysis rather than analytical measurements. Terms used for potato texture include flouriness, synonymous with mealiness (describing a dry, soft texture) and waxiness (describing a moist, firm texture). In addition, different consumer groups generally prefer different textures. For example, a dry boiled potato texture is preferred in Scotland, whereas a waxy texture is preferred in the Netherlands.

To establish an objective measure of potato texture a food texture analyser has been used for quantitative

texture measurement comparisons between Phureja and Tuberosum tubers. Results indicate that Phureja exhibits a very different boiled tuber texture, described as extremely floury or crumbly. In fact Phureja tubers cook in approximately half the time of typical Tuberosum samples (Fig. 5).

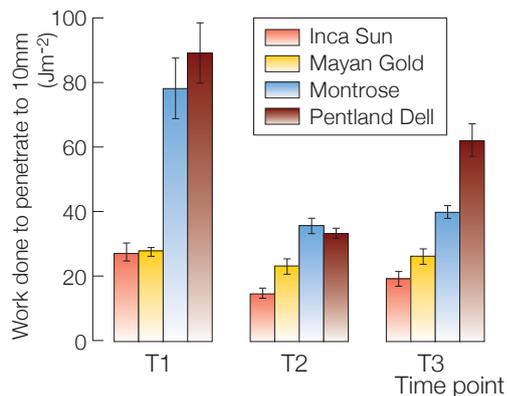


Figure 5 Texture Analysis of Tuberosum v Phureja T1: Developing tubers (30-50g), T2: Developing tubers (75-100g), T3: Mature tubers (150-250g), 2 weeks at 10°C. Each bar = mean of 8 tubers.

Factors that have an impact on cooked potato texture are likely to include starch content and distribution within the tuber, starch swelling properties, cell size, cell wall structure and composition and the breakdown of the cell wall middle lamella during cooking.

Recent research at SCRI has taken advantage of these potato types with very different tuber flavour and texture traits to begin to identify the genes underpinning these traits. We have used microarrays as a tool to identify genes with modified expression profiles that corresponded to differences in tuber flavour and texture. Gene expression was compared in two Phureja cultivars and two Tuberosum cultivars and showed that 309 genes were significantly and consistently up-regulated in Phureja, whereas 555 genes were down-regulated. Approximately 46% of the genes in these lists can be unambiguously annotated and identified, and amongst these are candidates that may underpin the differences between Phureja and Tuberosum with regard to flavour and texture traits. For example, a sesquiterpene synthase gene was identified as being more highly expressed in Phureja tubers.

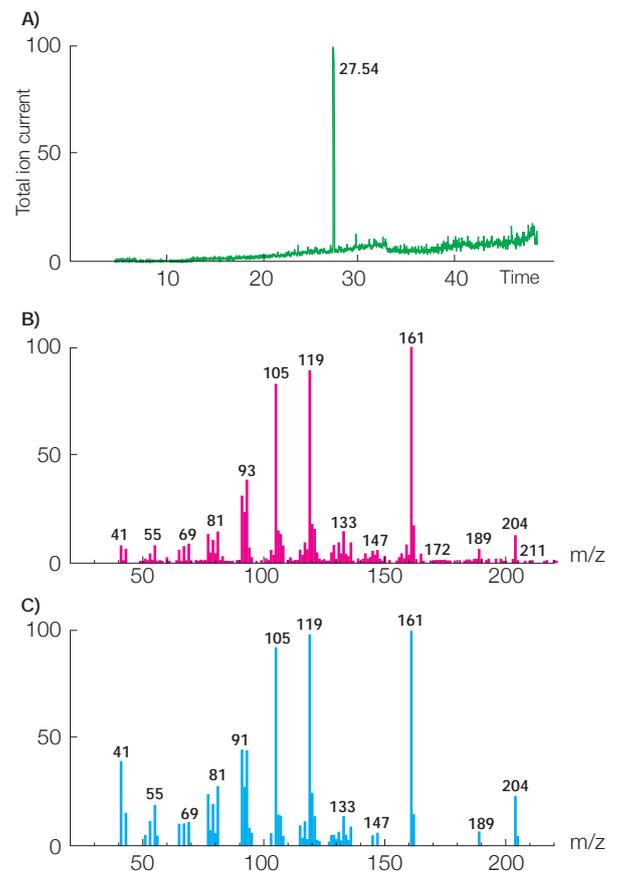


Figure 6 GC-MS analysis of the products produced by the putative sesquiterpene synthase. A – Total ion current trace. B – Mass spectra of peak at retention time 27.54min. C – Adam's library spectrum for α -copaene.

The gene was isolated and demonstrated to encode α -copaene synthase (Fig. 6). This correlates with the significantly higher level of α -copaene (a compound implicated in the 'baked' potato aroma) production from boiled Phureja compared with Tuberosum. Other potential 'flavour genes', identified from their differential expression profiles, include those encoding branched chain amino acid aminotransferase and a ribonuclease, which suggests a mechanism for umami-active 5'-ribonucleotide formation in potato tubers on cooking. Major differences in the expression levels of genes involved in cell wall biosynthesis (and potentially texture) were also identified, including genes encoding pectin acetyltransferase, xyloglucan endotransglycosylase and pectin methyltransferase.

In parallel with the molecular analysis of gene expression, biochemical analysis of cell walls from the Phureja and Tuberosum tubers revealed significant differences



Laurence Ducreux and Danny Cullen

that may contribute to the textural differences. For example, in the Phureja types, pectin is more easily solubilised from the cell walls and contains more methyl ester moieties than corresponding Tuberosum samples. Higher levels of pectin methylation have been previously correlated with enhanced cell separation and differences in texture on cooking in potato tubers. This result is also consistent with lower pectin methyltransferase gene expression and the levels of pectin methyltransferase enzyme activity found in the Phureja tubers. However, a role for starch in defining tuber textural properties cannot be discounted as starch rheology measurements and starch structural properties are also significantly different between the potato types.

To validate the role of these candidate genes in regulating flavour and texture we are manipulating the expression levels of these genes using transgenic

methods. For example, transgenic Tuberosum lines have been developed that produce significantly higher levels of α -copaene as a result of over-expression of α -copaene synthase. Sensory evaluation of these transgenic lines will be undertaken by international partners. Other transgenic lines are aimed at investigating the roles of the genes involved in pectin biosynthesis and the effect on texture and cell wall structure will be tested in the coming year.

To support these advances in the identification and development of quality, health and functional food components we have developed a range of high throughput analytical methods for their simultaneous detection and quantification. For example, as part of our fruit phytochemical studies, the inheritance of polyphenol components in the large progeny sets derived from the SCRI raspberry and blackcurrant

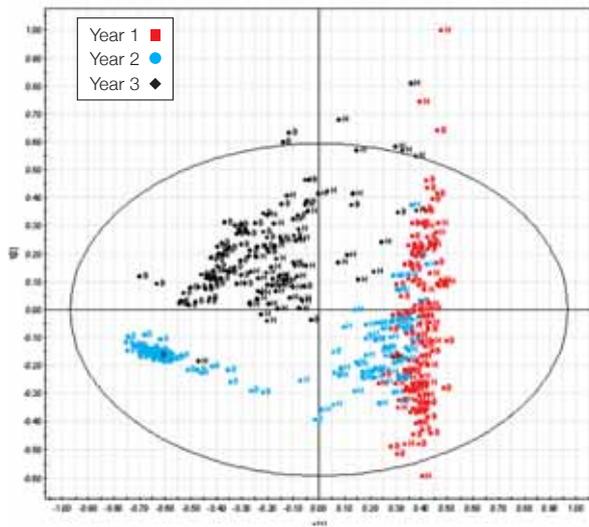


Figure 7 Metabolomics in action. Direct infusion mass spectrometric (DIMS) analysis of the fruit from the progeny of the Glen Moy x Latham raspberry cross grown in two environments (H and B) and over three years. The data (1600 mass spectral points per progeny and 5 replicates for every progeny) was then analysed by principal component analysis and the plot of score 1 v. 2 is shown above. This untargeted approach clearly shows that the fruit vary phytochemically year-on-year and that in year 2 the difference in environment was a dominant factor in determining the derivation of this difference.

genetic research required completely new approaches to data acquisition. These focus on the determination of key components using their characteristic mass spectroscopic signals and by deconvoluting the huge data sets using statistical methods. These methods are currently being validated and used to examine the importance of genotype \times environment interactions (Fig. 7).

The potential consequences of climate change form a basis for some of the programme's emerging research strands. Drought stress will be an inevitable global consequence of the predicted increase in climactic

extremes and is the focus for a collaborative project with The Irish Agriculture and Food Development Authority (TEAGASC). Currently a stepwise approach is being conducted to investigate the genetic basis of phenotypic and metabolic plasticity to drought stress in *Lolium perenne* L. (perennial ryegrass), an economically important crop for animal nutrition and the leisure industries.

A comprehensive metabolomic approach was carried out to elucidate the mechanisms involved in *L. perenne* response to drought stress. When leaf and root material from two genotypes, with a contrasting drought stress response, were analysed a clear difference was observed in the metabolic profiles of the leaf tissue under drought stress. Differences were principally due to a reduction in fatty acids levels in the more susceptible genotype (Cashel) and an increase in sugars and compatible solutes in the more tolerant genotype (PI 462336) in response to stress. The sugars significantly increased included raffinose, trehalose, glucose, fructose and maltose. Indeed, raffinose was identified as the metabolite with the largest accumulation under drought stress in the more tolerant genotype and may represent a target for selecting for superior drought tolerance into perennial ryegrass. The metabolomics approach is now being combined with the complementary transcriptomic study in the drought stress tolerant genotype PI 462336 and this has already identified several significantly up-regulated genes, such as fructan:fructan 6G-fructosyltransferase (6G-FFT), that corroborate the metabolomics and polysaccharide analytical findings and further add credence to the putative new targets for breeding.



Environment Plant Interactions

Philip White

Research in the EPI Programme seeks to describe, understand and predict how the environment impacts on plants, and how plants modify their environment – an environment that changes physically, chemically and biologically in both space and time. We focus on the efficient use of resources, such as light, carbon, water and minerals, and the development of sustainable and resilient arable ecosystems fit for global and environmental change.

The soil provides the substance in which plants grow and the mineral elements for their growth; it retains the water necessary for life, and contains the carbon to sustain the activities of micro organisms. “The nation that destroys its soil destroys itself,” said Franklin Roosevelt in 1937 when he urged state governors to adopt soil conservation laws at the end of the dust bowl. Seventy years on, soil degradation and its impact on global food production has prompted unprecedented media coverage of this most precious natural resource. In 2008, an issue of *National Geographic* was dedicated to soil, with articles describing the threats of erosion, drought and reduced fertility, the Royal Agricultural Society of England (RASE) published a report identifying the threat of soil degradation to food production, and the Scottish Government had

consultations to develop a ‘Scottish Soil Framework’ aiming to preserve the capacity of soil to produce crops and provide environmental services. Members of EPI are contributing significantly to improving the management of soil, through their work on ecological resilience and the alleviation of environmental constraints to crop production.

Future agroecosystems that deliver crop production with minimal environmental impacts require that the soil and biota, mineral inputs and losses to air and water all remain within specific bounds. Losses to the wider environment, in particular, need to be drastically reduced. In collaboration with colleagues at Warwick HRI, we have recently estimated phosphorus (P) loads to GB waters from agricultural sources to be 20% of the



Philip White

total P load, representing less than 3% of the P input to agriculture but still an important contribution to nutrient enrichment and eutrophication in surface waters. Similarly, in collaboration with the University of Aberdeen and SAC we have determined that nitrogen (N) fertilisers contribute most of the greenhouse gas (GHG) emissions from arable agriculture. Members of EPI are therefore developing strategies to reduce P and N

inputs to agriculture by improving fertiliser management techniques and by identifying genotypes with improved fertiliser acquisition and physiological use efficiency.

Liberty and limits to optimise agroecosystems To maintain agricultural production whilst improving ecosystem services, anthropogenic inputs, abiotic constraints and trophic interactions must be maintained within

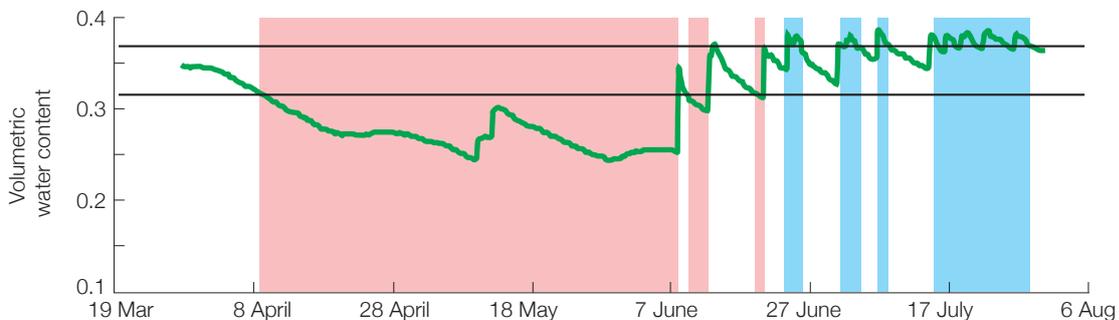


Figure 1 Variation in the volumetric water content of soil over time at SCRI showing periods when roots were likely to be limited by mechanical impedance (pink) and shortage of oxygen (blue).

appropriate ranges. Work in EPI has helped to identify these ranges, recently addressing various properties of soils, such as carbon content and compaction. For example, a least limiting water range can be defined for a soil, below which mechanical impedance or drought, and above which lack of oxygen, limit root growth. Even in the comparatively good soils of the SCRI farm, mechanical impedance restricted root growth in the dry period from April to May in 2008, and the subsequent, unforgettable rainfall raised water contents to risk levels for oxygen diffusion on four occasions, including one occasion lasting almost two weeks at the end of July (Fig. 1). A second example is that food webs must contain, or have available, a minimal carbon content for their upkeep. To enable soil micro organisms to carry out nutrient cycling and soil to remain stable, the carbon content in mineral soils should ideally be no lower than 2% of soil mass; a figure that is usually several times greater than the annual carbon intake by photosynthesis. Probably around 1–2% of the annual carbon budget is required in the form of wild arable plants to fuel the food webs of the soil surface and vegetation in the ploughed areas of field. As the total carbon is used, it needs to be replenished by additions in the form of roots and dead biomass. If the harvest takes too much material, or soils are repeatedly tilled, then the carbon content drops below the optimal range. Similarly, if the wild plants are removed, the arable food web will collapse.

There was great uncertainty, however, as to whether arable soils in Scotland were within 'safe' ranges for variables such as these. Essential baseline information was therefore gained through a major study on a total of 109 fields across 55 farms in the east of Scotland during 2007 and 2008. With SAC, arable fields were surveyed for soil properties, biodiversity, yield and agronomy, covering a wide range of management intensity and geographical location from Moray to the Borders. The results identified some worrying trends for arable east Scotland. Topsoils with carbon contents at or below a critical threshold of 2% were found on more than half the farms surveyed. A tenth of the topsoils sampled were highly compacted and susceptible to oxygen starvation when wet. Measurements of

penetration resistance suggested root elongation would be mechanically restricted in a third of all topsoils sampled. The low average soil carbon content and large physical resistance to root growth will have decreased primary production and crop yield below the climatic maximum. More nutrients need to be applied to such problem soils to achieve a given yield, while losses of nutrients to the air as greenhouse gas equivalents and to water through surface run off are both increased. Research in EPI is tackling these major problems through defining methods to improve the condition of soils and food webs and to raise the efficiency in the use of nutrients.

Sustainable mineral nutrition of crops In addition to oxygen, water and carbon dioxide, plants require 14 mineral elements. A lack of any of these impairs plant growth and crop yield. Mineral elements cannot be synthesised by a plant but must be acquired from the soil solution by its root system. Six mineral elements, N, P, potassium (K), calcium (Ca), magnesium (Mg) and sulphur (S), are required in large amounts. These are termed 'macronutrients' and supplied as inorganic fertilisers, mineral rocks or organic manures to maximise crop production. Other mineral elements must also be supplied to crops if they are lacking in the soil. Concentrations of mineral elements in plant tissues generally exceed those in the soil solution (Fig. 2) and this requires plants to invest energy into their acquisition.

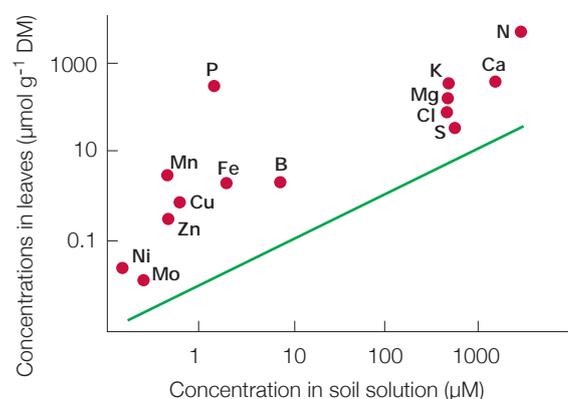


Figure 2 Concentrations of the 14 essential mineral elements in the soil solution and in leaves of plants. The line indicates equimolar concentrations in soil solution and plant leaves.



Phenotyping barley varieties.

The management of plant mineral nutrition is central to sustainable agriculture. Essential to the agricultural revolution was the synthesis of N-fertilisers from nitrogen in the air using the energy-driven Haber–Bosch process and the patented production of P-fertilisers from rock phosphates using sulphuric acid. However, the synthesis of N-fertiliser contributes significantly to

the production of GHGs, losses of N and P from agricultural land contribute to the processes of eutrophication, and it has been estimated that commercially viable sources of P and S will be exhausted within 50 years. For all these reasons, alternative sources, and effective recycling, of mineral elements for agricultural production must be found.

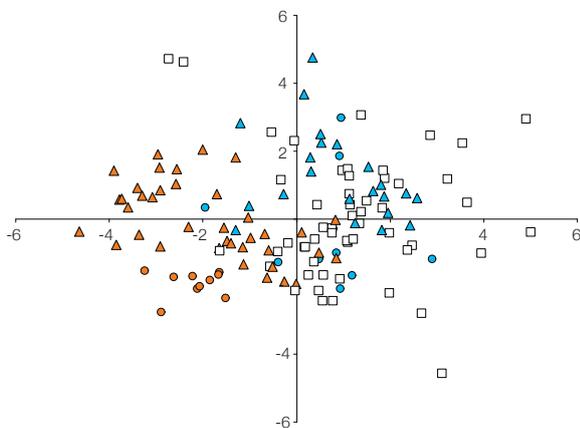


Figure 3 Phenotyping barley varieties for plant development and nutrient use and statistical plot (principal components analysis, PCA) derived from phenotypic data showing separation between two sets of mutant lines (blue and orange) and commercial varieties (white).

In EPI, we are pursuing two complementary approaches towards sustainable mineral nutrition of crops. The first is agronomic, where we aim to minimise the application of conventional inorganic fertilisers through soil management, fertiliser-placement, scheduling and decision support techniques. Employing these techniques in an integrated farming system could halve the fertiliser burden. We consider the agronomic approach to lead to the greatest improvements in the shortest time. The second approach is through genetics and is founded on the observation that crops that yield best with reduced fertiliser inputs are those whose roots acquire mineral elements from the soil most effectively and produce higher yields from a given plant nutrient content.

Historically, the application of agronomy and genetics to intensive agriculture has attempted to maximise specific aspects of crop physiology, such as the rapid expansion of leaves or the partitioning of biomass from foliage to seed. In many environments, however, plants are subject to multiple constraints and phenotypic specialisation tends to render them more susceptible to acute stress at some point during their life cycle. We are therefore working through concepts, experiments and models to enable the design of plants and crop systems in which the underlying components of survival, growth and fecundity are balanced and the resulting plants and crops are more resilient to environmental change.

Harnessing genetic variation We are studying genotypic variation, environmental plasticity, and the genetic basis of important traits and processes including root system architecture, the root–shoot balance, the uptake and use of mineral elements, biochemical processes that increase the availability of mineral elements in the soil and tolerance to abiotic stress (Fig. 3). New methodologies are being developed. For instance, a four-year collaboration with the universities of Cambridge and Dundee has produced PlantVis, in which confocal microscopy is combined with image analysis to identify growth parameters in specific root zones at cellular resolution (Fig. 4). Using these and other methods, we have identified large between-species and within-species genetic variation in many relevant traits. Ample genetic variation has been found in barley for traits which affect growth in compacted soil and the acqui-

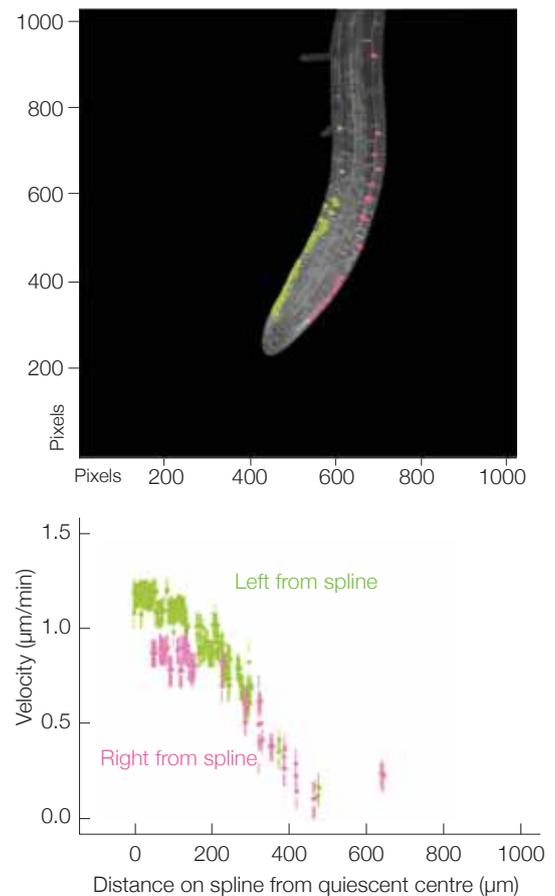


Figure 4 Sensitive image analysis tool (PlantVis) developed in collaboration with the University of Dundee for estimating motion in living organs: examples show (upper) image of growing root with two areas selected for estimating growth rates, and (lower) the velocity of these expanding regions relative to the distance from the quiescent centre. Spline = line drawn through the central longitudinal axis of root.

sition of water and minerals. In the field, a screening approach has been developed to identify barley genotypes that have a greater capacity to discover biopores that serve as conduits across mechanically impeded plough-pans, providing rapid growth pathways to otherwise inaccessible resources. Over 50 barley lines have been tested in EPI's long term tillage experiment which compares direct drilling, minimum tillage, ploughing or deep ploughing. Several promising genotypes have been identified that could be developed for farming systems employing reduced tillage.

Chromosomal loci and genes have been identified that increase the acquisition of mineral macronutrients from both conventional and alternative fertilisers



Figure 5 Aerial photograph of a field experimental site where the effects of compost and slurry amendments to soil are being investigated.

and that improve the physiological use efficiency of mineral macronutrients in brassica, cereal and potato crops. While such information is valuable to breeding programmes, genetic contributions to resource acquisition are often complex and environmentally-dependent, since plants employ combinations of diverse strategies to optimise their acquisition of water and mineral elements. Plant husbandry and fertiliser management must also be considered therefore, when producing crops that use water and fertilisers most effectively.

Field management for offtake, food quality and sustainability

Carefully targeted additions or interventions can often lead to rapid beneficial change. Here are two examples of the way EPI is taking research to practice. In the first, methods are being developed to supplement, or replace, inorganic fertilisers with alternative fertilisers, such as composts from urban green wastes, animal manures and struvite (an abundant ammonium magnesium phosphate reclaimed from sewage). We are also investigating the use of legumes and microbial inoculants to improve the availability of essential mineral elements. A major development this year has been to test quality composts made from urban green wastes (the cuttings, clippings and weeds from gardens and public spaces). These soil amendments can restore some of the carbon and nitrogen lost from soils and improve their structure, water retention and workability. Supported by the Waste and Resources Action Programme (WRAP), we have established long term field trials studying the effects of these amendments on yield and quality of barley and

potatoes in both conventional and organic systems (Fig. 5). Increased yields and improved product quality were found when these amendments were used as supplementary fertilisers.

The second example contributes more directly to the topic of human health. Humans require more than 22 mineral elements for their wellbeing, one of which is selenium (Se). Dietary Se intakes in the UK have declined to almost half the 1970s level, in part, a consequence of replacing North American milling wheat, which is grown on high Se soils and has a high Se concentration, with wheat grown in low Se soils of the UK. A collaboration with members of the Defra LINK BAGELS Consortium (University of Nottingham, University of East Anglia, Rothamsted Research, Institute of Food Research, Nickerson-Advanta, Velcourt, Carrs Fertiliser, Yara UK and Marks & Spencer) demonstrated that the application of Se-fertilisers to wheat crops grown in the UK increases their grain Se concentrations without affecting other quality attributes important for breadmaking. Loaves baked from this Se biofortified UK wheat, in which one slice delivered approximately 10% of the recommended daily intake, were produced by Marks & Spencer and distributed to visitors to the Cereals2008 event in Cambridgeshire.

Designing plant–soil systems for better capture and use of resources

EPI is developing a strong capability in ecosystem design, combining knowledge at different

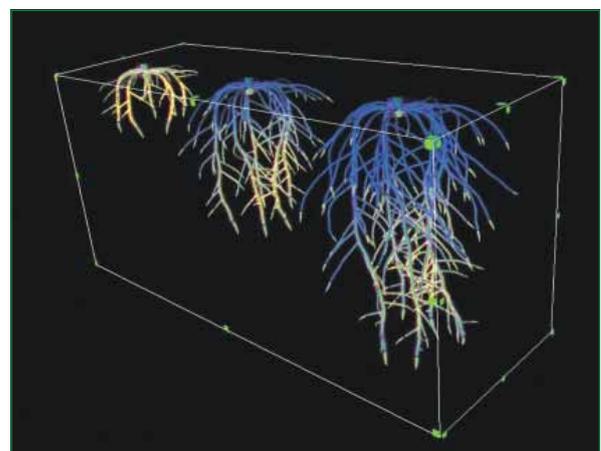


Figure 6 Computer generated figure of the three dimensional growth of a root system over time, showing the evolving regions of active nutrient uptake (yellow) and the structural framework (blue).

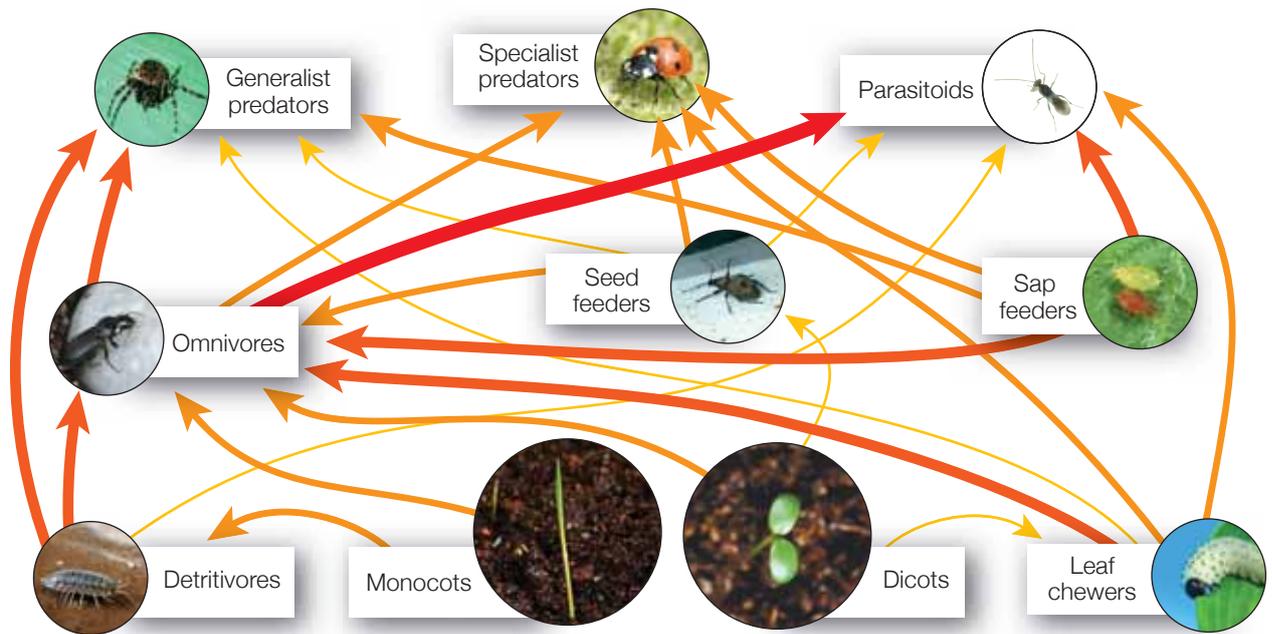


Figure 7 Schematic illustration of the main functional components of the within field arable food web based on monocot (grasses) and dicot (broadleaf) arable plants. The thickness of a line indicates the strength of the relationships between each functional group.

biological scales from the plant to the landscape to devise systems better able to meet the challenges of the future. Designs are being tested experimentally in controlled environment rooms, glasshouses and field plots. Testing will soon move to SCRI's new long term, field scale experimental platform at Balruddery Farm. Here, we give two examples of our work on system design – one for plant roots and one for the essential biodiversity in an arable production system.

Models of growing root systems are constructed to optimise the uptake of nutrients by plants and thereby reduce the input of fertiliser. The models incorporate genetically controlled mechanisms by which the plant senses and responds to environmental signals (Fig. 6). The models integrate the couplings between the biophysics of root–soil interactions, the physiology of the whole plant and the genetic control of growth and development. These structure–function models will ultimately be used to guide both the selection and breeding of crop varieties, the choice of a crop suited to local constraints and the adaptation of agronomic practice to reduce inputs.

At a larger scale, cropping systems are being designed that adopt new, more profitable crops but avoid any

undesirable effects on the essential biodiversity that maintains the soil and field. A food web for the arable system has been constructed from field data (Fig. 7). A mathematical model of this food web, developed with Rothamsted Research and Syngenta through the Sustainable Arable LINK programme, is being used to assess the effect of a change in crop genotype or management on the partition of energy and matter among crops, wild plants and invertebrates. A change that reduces the important organisms below defined limits will be discouraged. Finally, the environmental and associated economic factors consequent on various options and scenarios are being examined with stakeholders using multi-attribute decision models (MADMs) developed with the Josef Stefan Institute, Slovenia.

Through its innovative, holistic research and system design, EPI is ideally placed to inform government and the public on the major challenges of the coming decades. Its expertise and contributions are central to predicting and adapting to global change, enhancing and preserving essential biodiversity in and around farmed landscapes and producing nutritious food in a sustainable way.



Division of Plant Sciences University of Dundee

John W. S. Brown

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

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

and exploit opportunities for interaction to benefit both organisations.

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



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

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

Plant pathogen effector delivery (Paul Birch) Plants face a constant barrage of invading microorganisms, including bacteria, fungi and oomycetes. They are able to detect these invasions and respond with rapid activation of a range of defences which are effective in preventing disease in the majority of cases. Successful pathogens secrete proteins called effectors that act either outside or inside host plant cells to manipulate key defence components and promote susceptibility to infection. The oomycete *Phytophthora infestans* causes the devastating disease late blight that remains the greatest constraint, globally, to potato production. It secretes



Paul Birch and Emma Douglas

effectors containing a motif, RXLR, which we have shown is required for these proteins to enter host cells. We have demonstrated that, although these proteins presumably suppress host defences, some of them are detected by co-evolving resistance proteins in the cytoplasm of some plant genotypes. Such molecular recognition results in host cell suicide, preventing the pathogen from spreading further in the plant. There are potentially >400 such effectors produced by *P. infestans*, suggesting that molecular interactions with the host are highly complex to evade detection and establish a successful infection. In the coming years we will explore the function, localisation and delivery of the RXLR effectors in detail.



John Brown and Morven Pearson

The nucleolus and pre-mRNA processing (John Brown) When genes are expressed, they are copied into precursor messenger RNA (pre-mRNA) and introns are removed by splicing. Errors in transcription or splicing generate inaccurately spliced mRNAs which are detected by the cell and degraded. This process is called mRNA surveillance or mRNA quality control. The finding that proteins which are normally associated with mRNAs were present in the major sub-compartment of the nucleus – the nucleolus – suggested that mRNAs might also be present here. The nucleolus is now known to be multifunctional and involved in many aspects of RNA processing but is not generally thought to be involved in mRNA processing. We have now shown that the nucleolus is enriched in mRNAs which are improperly processed. The nucleolar mRNAs contain unspliced introns, unusual splicing events and some known alternatively spliced events. More importantly,

the majority contain signals which would be detected by the mRNA surveillance machinery and we have shown that many are indeed degraded. This unique finding suggests that the nucleolus in plants has a function in mRNA surveillance. Using mutants in *Arabidopsis* and the RT-PCR alternative splicing panel which we have developed, we will now investigate how and where aberrant mRNAs are detected and degraded.

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



Sujatha Manthri

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



Division of Plant Sciences laboratory



Abbey Barakate and Claire Halpin

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

Understanding and manipulating lignin biosynthesis

(Claire Halpin) Over the past 15 years a huge amount of research, including work from my laboratory, has gone into understanding the pathway/genes that control lignin biosynthesis in plant secondary cell walls. The lignin pathway is now probably one of the best understood plant metabolic pathways. This is fortunate, as lignin is a major target for manipulation to improve plant raw materials as feedstocks for bioenergy production. Increasing concerns about rising CO₂, climate change, and the finite nature of oil supplies, has renewed interest in plant biomass as an alternative energy source. Plant biomass can produce energy either directly, by burning it, or by using it as the raw material from which bacteria and yeasts can produce biofuels. Currently, bioethanol

is produced from high sugar plant materials such as grain, and has led to much debate on the issue of 'food v. fuel'. However, the rational way to make biofuel without depleting food stocks is to use non food parts of plants (for example, waste straw). In many plants, more sugar substrate for biofuel production is locked up in the cell walls of vegetative tissues (stalks, leaves) than is present in the grain, but this sugar is hard to release due to the presence of lignin. This is where detailed knowledge of the biochemistry and molecular biology of lignin production, achieved by many years of basic research, can be brought to bear on this significant industrial and environmental problem. We have several projects about to start (funded by European Union (EU), Biotechnology and Biological Sciences Research Council (BBSRC) and Global Climate and Energy Project (GCEP) at Stanford University, USA) that aim to determine how lignin can be manipulated to allow efficient production of biofuel from substrates such as barley straw. This work will benefit enormously from the barley genetic resources available at SCRI and will further our collaboration with Genetics and PPFQ.

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

To identify useful gene alleles we use high throughput molecular markers, including the Illumina Oligo Pool Array, which has been pioneered in barley by the SCRI Genetics programme and has already been

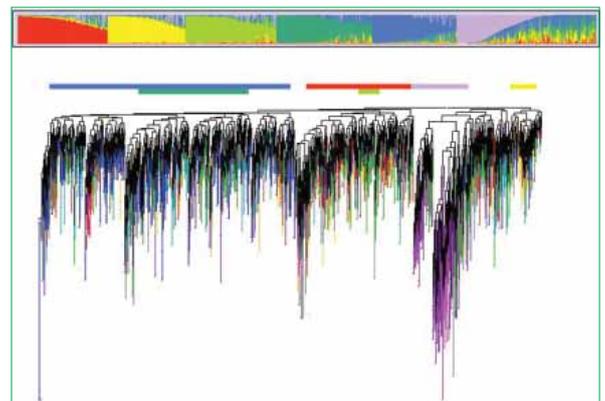


Figure 1 Genetic diversity of 3000 pea samples. Top: Species structure – each sample is represented as a vertical line comprised of a combination six colour-coded 'ancestral genotypes'. Bottom: Family tree - using the same colours as the structure chart. Wild peas are almost all in the lilac region of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

used successfully for discovering useful marker–trait associations in barley cultivar germplasm. We are working with Genetics and the European barley community to extend these studies to landraces and wild plants to identify new alleles. Lastly, we are working with SCRI Bioinformatics staff to develop the Germinate



Andy Flavell



Steve Hubbard

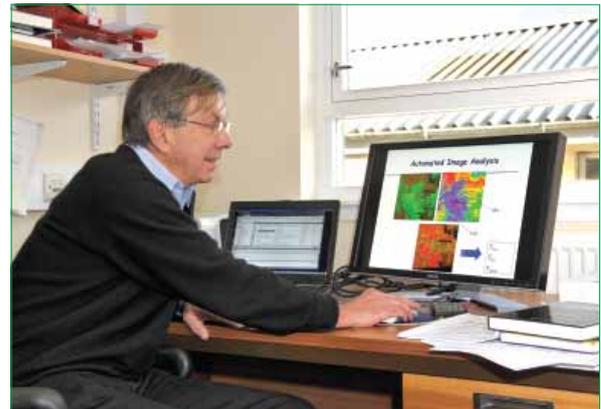
database to store, analyse and visualise the huge amounts of data created by the above approaches.

Relationships between insect parasitoids and their

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

Most aphid species possess an obligate primary bacterial endosymbiont, *Buchnera aphidicola*, and one-to-several types of facultative bacterial endosymbionts (secondary symbionts) that are members of the γ -proteobacterial family, the Enterobacteriaceae. *Buchnera* synthesises essential amino acids, thus providing aphids with nutrients that are poorly represented in plant phloem sap, and also encodes a chaperonin protein that facilitates transmission of circulative plant viruses by a number of aphid species. The role of secondary symbionts is less well

characterised, particularly with respect to aphid vector competence, and has largely been investigated in the pea aphid (*Acyrtosiphon pisum*) where they have conditionally beneficial or deleterious effects on aphid performance and aphid-natural enemy interactions. Our current research aims to investigate the roles of plant, parasitoids and symbiotic microorganisms on the capacity of aphids to vector plant viruses.



Lyn Jones

Plant ecophysiology and adaptation to environmental

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

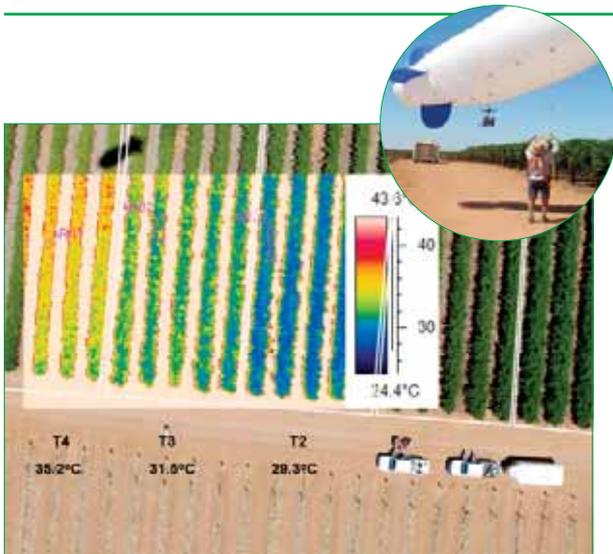


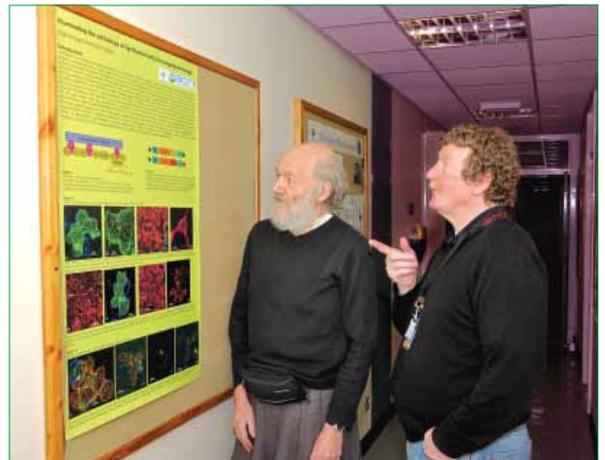
Figure 2 Oxford Landing vineyard (Australia) from a helium balloon (inset) - overlaid thermogram showing substantial increases in canopy temperature as the amount of irrigation decreases (original pictures from Ashley Wheaton).

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



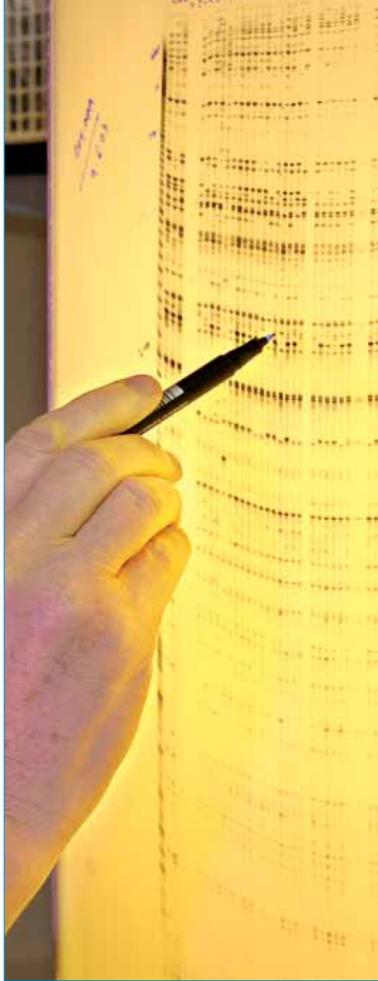
Figure 3 Cylindrical cells of *Coscinodiscus wailesii* (end view) and a cell division (side view) with cells about to separate. Cell diameter 0.4 mm; cell height 0.2 mm.

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



John Raven and John Brown

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



Biomathematics and Statistics Scotland

David A. Elston

Biomathematics and Statistics Scotland (BioSS; www.bioss.ac.uk) is a specialist organisation delivering 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.

BioSS manages its consultancy work under 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 a smaller number of deep, collaborative relationships.

Our ability to support a large portfolio of projects in these four application areas is greatly enhanced by our training courses in quantitative methodologies. These courses

increase the understanding and computational abilities of our collaborators, enabling them to perform many analyses with minimal guidance and to discuss their projects with BioSS consultants at a higher level.

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

- statistical bioinformatics
- systems and 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, demonstrating the wide applicability of BioSS research.



BioSS inputs to microarray experiments (Christine Hackett, Chris Glasbey, Graham Horgan, Mizanur Khondoker, Claus-Dieter Mayer & Jim McNicol)

Microarrays are one of the many remarkable tools that enable us to probe ever deeper into the molecular activity taking place within the cells of all living organisms. Whilst microarray technology continues to advance, the quantitative issues raised are generic, and the progress we have made in addressing these issues demonstrates the interplay between BioSS research and consultancy. To simplify the exposition, we consider two colour microarrays, each of which contains spots of cDNA from 10,000s of genes. Extracts from two samples (for example, individual plants or bacterial cultures) are applied to every spot on a given array, and the intensity of colour of each of two dyes on these spots records the levels of gene expression associated with each sample. The samples can be chosen to allow us to find out about expression levels associated with particular types of individuals (different varieties, experimental treatment groups, or varying according to a quantitative trait such as weight). Irrespective of the many variations, microarrays enable scientists to measure the expression of thousands of genes simultaneously, leading to enormously high dimensional data, posing challenges for design and analysis that have been addressed in complementary ways by BioSS staff in Edinburgh, Aberdeen and Dundee.

Design Differences in expression levels between pairs of samples applied to the same array are estimated much more precisely than differences between arrays, hence a key decision in the design of two colour microarrays is the specification of such pairs. Early experiments favoured the so-called reference design in which all samples were compared to a single reference or control sample (for example, [A,R], [B,R], [C,R]). As this only allows indirect comparison of pairs not including the reference sample (for example, [A,B]), more general designs like loop designs (for example, [A,B], [B,C]... [Z,A]) have also been used which allows some comparisons to be estimated with increased precision.

Our work on the design of microarray studies has been to capitalise on information about the samples in two

different settings. The first setting is where we have measured a single quantitative trait on each sample and wish to estimate a linear regression between trait values and expression level. We have demonstrated the benefits of ranking the samples in both directions (highest to lowest and lowest to highest), then constructing a loop design which uses pairs of approximately the same rank in the opposite direction. Furthermore, we have established the situations in which additional replication of samples with extreme trait values, at the expense of samples with trait values close to the mean, can be beneficial.

The second setting is where we have information about a large number of genetic markers for each sample. We have investigated the construction of distant pair designs in which the aggregate number of discrepancies between markers within pairs is as large as possible. We have written a computer programme to optimise this criterion for a barley population, using simulated annealing.

Preprocessing Microarray data in raw form almost inevitably contain artefacts due to imperfections in the technology which, if not addressed properly, can obscure biological signals. Preprocessing is therefore a key step in analysis, which BioSS has advanced through *combining multiple laser scans* and using nonparametric methods for *normalisations*.

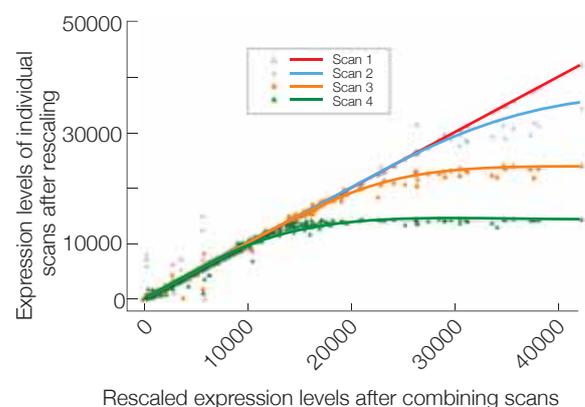


Figure 1 Example of rescaled multiple scan data with fitted nonlinear functional regression model shown by solid lines. Data from different scans with incremental PMT settings are related nonlinearly due to variant amounts of signal saturation.

Combining multiple scans Expression data for analysis are typically derived from a single laser scan of each hybridised cDNA microarray. However, because weakly expressed genes are better measured at high photo-multiplier tube (PMT) gain settings and highly expressed genes at low settings (Fig. 1), there are benefits in combining scans to obtain more sensitive data across the range of expression levels. We have developed a nonlinear functional regression model with errors based on the heavy-tailed Cauchy distribution for robustly estimating gene expression. Software is available via a web interface: www.bioss.ac.uk/ktshowcase/create.cgi

Normalisation is the process of removing systematic variation so that data from different microarrays are on a common scale. There are two main aspects: location normalisation to remove biases in mean expression levels, and scale normalisations to remove differences in the spread of observed expressions for given mean values. Typically, nonparametric methods such as *loess* are used for location normalisation and parametric transformations such as *arcsinh* for variance stabilisation. However as can be seen in Fig. 2a, patterns of variation are typically too complex to be adequately modelled parametrically.

We proposed a new normalisation method using a generalised additive model for location, scale and shape (GAMLSS; Fig. 2b). Simulation studies show that GAMLSS normalisation yields more powerful inference of differential expression than the standard parametric method.

Analysis The first analysis step following the normalisation is to find genes that exhibit evidence for differential expression. The standard statistical approach here is to apply a test for each gene, using data from that gene alone. As most microarray experiments tend to have small sample sizes, the estimate of the standard errors used in such tests will not be precise. For genes with small observed standard errors this value will tend to have been underestimated, leading to false positives, whereas for genes with large observed standard errors this value will tend to have been overestimated, leading to false negatives.

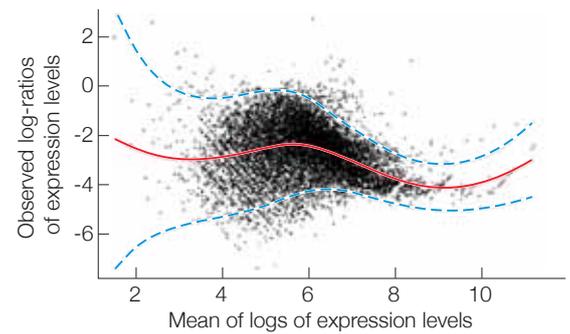


Figure 2a GAMLSS fit to data from a single microarray, showing the log-ratio of the observed colour intensities of the two samples for each gene plotted against the average of the two log intensities. The solid red line shows the location model and the blue dashed lines show the spread ascribed by the scale model.

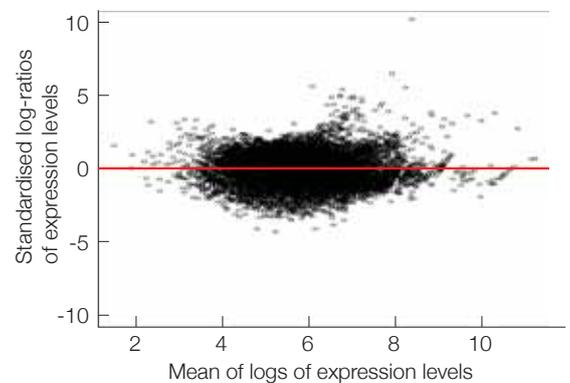


Figure 2b GAMLSS normalised log-ratio plotted against mean log-intensity (x). As intended, the majority of the normalised data (corresponding to genes not showing differential expression) are symmetrically distributed around the zero reference line and have homogeneous variability over the range of mean intensities.

For this reason we use *moderated t-tests* for comparisons of mean expressions in two treatment groups, and equivalent analyses for more complex designs. The process of moderation shrinks the standard error for each gene towards the average standard error observed across all genes to stabilise the analysis. For each gene we obtain a p -value which quantifies the statistical significance of the observed difference (technically, the probability of obtaining a test statistic as extreme as that observed if there were no true effect).

False discovery rate The next step is generally to select a cutoff, p_c , and declare that we have 'discovered' evidence of differential expression for all genes with p -values smaller than p_c . The value of p_c can be



David Elston

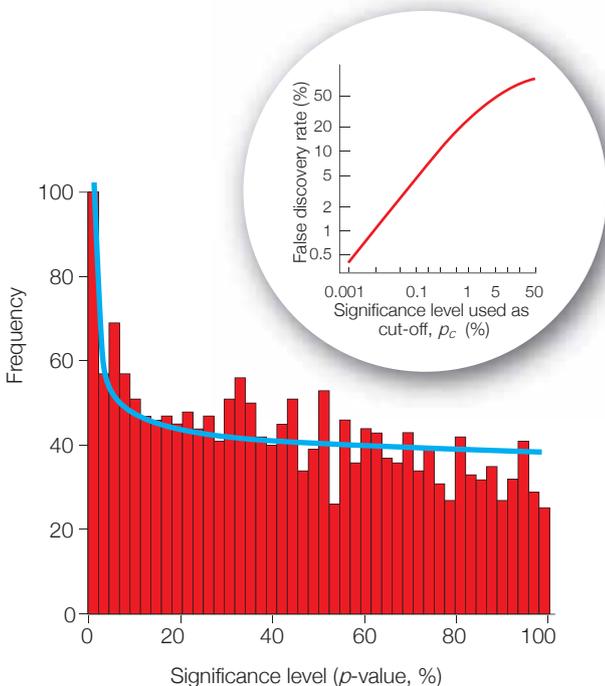


Figure 3 Observed (histogram) and modelled (solid blue line) distributions of significance levels for differential expressions of individual genes, together with (inset) the modelled relationship between gram false discovery rates (FDR) as a function of the significance level used as cut-off, p_c .

thought of as the false positive rate (the probability that a gene without differential expression gets incorrectly 'discovered'). Because the expression levels of so many genes are estimated in each microarray experiment, it is important also to know the proportion of discoveries which are likely to be false. This is the false discovery rate (FDR). The FDR associated with any value of p_c is estimated by modelling the distribution of p -values. Fig. 3 shows an example in which a significance cut-off of 5% corresponds to a FDR estimate close to 50%. The FDR estimate makes us wary of using 5% as a significance cut-off. With this data set, a FDR of 1% would need a p_c -value of around 0.005%.

Identification of regions controlling expression: eQTL analysis Microarrays provide an opportunity to merge the analysis of gene expression data with information on chromosome position provided by DNA markers. Typically such an analysis is carried out using data from a segregating population of offspring obtained from crossing two inbred parents. The outcome is an estimate of the regions of the genome controlling expression of each gene on the microarray.

Often, the locations of many of the genes on the microarray are known and the region associated with gene expression includes the known gene location (referred to as a *cis*-regulated gene). However, the region controlling gene expression is sometimes found to be separate from the gene location (referred to as *trans*-regulation). These sites may be major gene regulators, playing a central role in the molecular

interactions taking place within cells and ultimately having effects on many traits exhibited by whole organisms. This information is currently being used by scientists working on completely sequenced species such as *Arabidopsis* to build gene regulatory networks, and should soon become more feasible in crop species such as barley.

Climate change research at SCRI

Adrian C. Newton

Climate change is widely recognised as the most serious environmental threat facing the world today and is becoming central to policy making and land use decision-making. The climate change predictions for Scotland include increased temperatures, seasonal changes in precipitation patterns resulting in both drought and flooding/waterlogging, longer growing seasons and more extreme weather events. The Scottish Government has set ambitious targets in its Climate Change Strategy, announcing a proposed target for reduction of greenhouse gas (GHG) emissions of 80% by 2050. Much of the science research being carried out at SCRI is about providing the tools and resources for both mitigating climate change and adapting to its consequences, essential components of the strategies which must be implemented to achieve these policy targets. In many respects climate change related research is what we have been carrying out successfully for many years which has advanced the utility of our crops. However, recognition of the global

nature of the change, its man-made cause and the enormous scale and seriousness of the consequences has reemphasised the importance of developing sustainable and resilient solutions to the environmental changes we are likely to face.

Our climate in Scotland has been changing in line with the overall trend; with a mean temperature rise over the last 40 years of about 1.2°C. On the main Mylnfield SCRI site, climate measurements have been made continuously since 1959, and whilst much of the data collected is standard, it includes measurements of soil temperature at 10, 20, 30, 50 and 100cm depths and clearly demonstrates that even the subsoil is warming. This may have profound implications for the biological processes involved in carbon cycling in soils and therefore the long term health of our crop land. This is linked with other work on carbon additions to our soil using farmyard manure and municipal compost, the latter offering a potentially important means of mitigation whilst improving our crop soil. (Fig. 1) The amount of root left in the soil by crops varies with genotype and this is being studied both in controlled environments and non-destructively in the field for barley. As barley dominates the arable rotation in Scotland, this could have important implications for carbon sequestration.

The consequences of climate change, particularly milder winters, are already being seen in our blackcurrant crops where lack of winter chill results in asynchronous development, more specifically uneven budbreak and subsequently uneven ripening. In a crop which relies on machine harvesting on one occasion, this can cause severe reduction of both quality and yield. The identification of phenotypic variation in chilling requirement and understanding the molecular

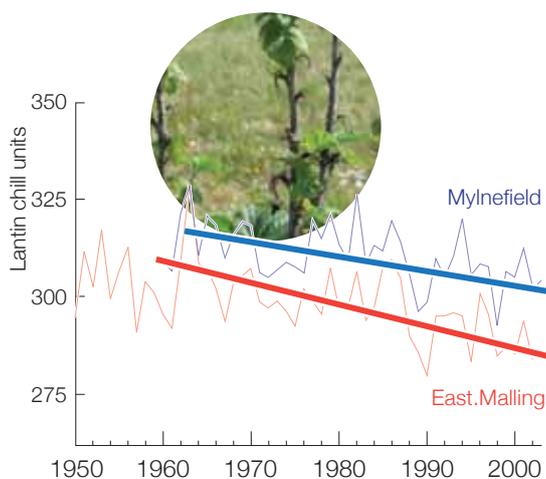


Figure 1 Comparison of long term trends data in the north and south of the UK.

mechanisms controlling related processes such as dormancy release are key objectives of our research. In barley the genetic and molecular basis of control of developmental processes affected by the stresses likely to increase with climate change are similarly the focus of research projects. For example, alternative gene splice events may occur in response to stresses resulting in different gene products being made. In the case of both blackcurrant and barley research, the principles and mechanisms identified which can be manipulated in breeding are not only useful for adapting these crops to climate change, but potentially other woody perennials and cereals respectively

Pests and pathogens are organisms which are specifically adapted to exploit resources not adequately protected by plant defence mechanisms. Climate change will open new opportunities for these organisms and the populations of the peach potato aphid (*Mysus persicae*), the potato late blight pathogen (*Phytophthora infestans*) and other pathogens are being monitored in detail both quantitatively and by studying the genotypic structure of their populations to determine how much climate is driving changes, and how much is driven by factors such as varieties, agronomic practice and agrochemical control measures. These threats feature strongly in an assessment of the likely changes in pest and pathogen challenges, particularly the possible effects of climate change on aphid populations transmitting viruses to potatoes, as the virus-free status of the Scottish seed potato industry is crucial and could be threatened. Solutions via both breeding for resistance and development of crop protection methodologies are central to our research and integrating these with continued improvements in quality and yield in new cultivars is pursued through networks with plant breeders.

Climate change has implications for yield and quality too, often likely to be negatively affected either directly or from increased or changed pest and pathogen attacks. Moreover effects are likely to be less predictable as a consequence of changed precipitation patterns and more extreme weather events. Furthermore, effects of climate change on one organism may have



Controlled growth chamber with elevated CO₂.

unpredictable consequences for secondary and tertiary trophic levels. An example of this is shown in work carried out in our elevated CO₂ chambers on a legume and insect interaction. Under 700 $\mu\text{l l}^{-1}$ CO₂ the number of root nodules increases, but so does the number *Sitona lepidus* larvae which target root nodules resulting in reduced root nitrogen per unit root dry mass.

SCRI leads the Scottish Government Rural & Environment Research and Analysis Directorate's (RERAD) Programme 1: Profitable and sustainable agriculture: plants, which has three cross-cutting themes, one of which is 'Responding to Climate Change'. Whilst we report progress of research within the theme in the context of this programme, we are increasingly moving towards work which examines the effects of climate change on all land use issues which crosses this, other commissioned research programmes and beyond since, just as climate is a complex system, so must our response be. Together with the other Main Research Providers we address not only the biological interactions, but also the socio-economic implications of adaptation and mitigation actions to direct our research priorities. Future work will be increasingly cross-disciplinary and require joint climate change research facilities which are currently being planned.

Balruddery Farm :

arable sustainability in theory and practice

Cathy Hawes, Euan Caldwell, Peter Gill & David Hopkins

Over the past half a century intensification of crop production, often solely for economic gain, has led to the systematic erosion of arable biodiversity and the degradation of arable habitats in many parts of the world. This has raised serious concerns about sustainability and long term food security, particularly where intensive management has had negative impacts on the functioning of agricultural systems.

Arable sustainability is the ability of a system to maintain stable levels of food production and quality in the long term without escalating requirements for agrochemical inputs to regulate the system. To achieve this, the within field arable habitat should be able to support stable populations of a range of organisms that regulate key system processes (primary production, nutrient cycling, decomposition, predation and pollination). Management

for arable sustainability must therefore allow coexistence of different functional groups of plants and animals, and the use of crop varieties that can tolerate a degree of weed, pest and disease pressure.

Balancing food production and environmental sustainability is central to the principles of the LEAF (Linking Environment and Farming) organisation. SCRI has been a LEAF Innovation Centre since 2004 and is one of only two such centres in Scotland. The purchase of Balruddery Farm represents a unique opportunity to expand and develop SCRI's role as an Innovation Centre. LEAF is "committed to a viable agriculture which is environmentally and socially acceptable and ensures the continuity of supply of wholesome, affordable food while conserving and enhancing the fabric and wildlife of the countryside for future generations" (www.leafuk.org).



Balruddery Farm is an 118 ha arable farm located seven miles west of Dundee and between 70 and 160m above sea level on the lower slopes of the Sidlaw Hills. There are 17 fields varying in size from 2.0 ha to 11 ha. The soil is a sandy loam, slightly shallow in depth on the eastern fringes adjacent to Balruddery Den. The farm is fairly typical of the area, with field boundaries being marked by drystone dykes and the wooded den of the Balruddery Burn on the eastern boundary. There are mature tree lines and an old hedgerow along some of the dykes and two smaller watercourses that run west to east across the farm and feed into the West Den of Balruddery. The farm has previously grown oilseed rape, potatoes, barley, wheat and grass.



Plans for developing Balruddery Farm as a LEAF Innovation Centre include: regenerating existing hedgerows to provide a wildlife corridor running east-west across the farm, linking with woodland habitats on either side; increasing margin widths to at least 2m to buffer farm habitats from field operations; increasing buffer strips along water courses to 6m (a current Government proposal with the ending of set aside), and; establishing wildflower populations in field corners and edges to encourage pollinators and natural enemies.

SCRI can contribute to these goals through specific sustainability research programmes and through the adoption of LEAF recommendations for environmental

management of the marginal land and the non-trial break crops within the rotation. A plant and invertebrate monitoring programme will be established in 2009



Within-field habitats are as important as the field margins for arable biodiversity and ecosystem functioning. Opportunities to follow LEAF guidelines for the management of these habitats at Balruddery Farm include leaving over-wintering stubbles to provide feeding areas for farmland birds, establishing conservation headlands on one side of each field during the break years between barley and potato trials, introducing beetle banks to encourage predators and planting bird cover crops.



Figure 1 Current research at SCRI on sustainability includes screening crop varieties for nutrient use efficiency (left: potatoes in the Commonwealth Potato Collection show variation in micro-nutrient use efficiency), developing methods for enhancing resistance to pests and diseases (middle: barley cultivar diversity is used to reduce the spread of *Rynchosporium*), and assessing management impacts on biodiversity and resilience (right: surveys of LEAF, organic and conventional farms with different levels of management intensity).

to assess the efficacy of these LEAF management guidelines on long term trends in biodiversity at the farm.

Research at SCRI focuses on developing crops and crop management to enhance the sustainability of food production (Fig. 1). Crop traits are being identified that can improve stress tolerance and the efficiency of water, light and nutrient resource use, all of which result in the opportunity for reducing inputs and improving environmental and economic sustainability. Sustainable crop protection practices are also being developed that focus on environmentally benign and cost effective ways to reduce the incidence and severity of crop pests and diseases. Finally, soil and weed management strategies are being investigated to determine the optimal combination of management and crop variety for high yields whilst maintaining the biophysical resilience and ecological sustainability of arable systems.

We are now in a strong position to build on this research and develop an integrated approach for testing the results and hypotheses arising from these studies within the context of the whole within field arable ecosystem.

To do this, a research platform will be established at Balruddery Farm for long term studies on arable sustainability. The overall goal is to test whether or not potential solutions for sustainable agriculture arising from the current RERAD research programme, actually result in improved arable biodiversity, resilience, crop productivity and yield stability at a commercial field

scale over at least four rotation cycles. A 'sustainable' cropping system will be designed that we predict will optimise inputs, yield, biodiversity and ecosystem processes. The effect of this 'sustainable' system on long term trends in yield and system health will be tested by comparison with current commercial practice. This research platform will provide a test-bed for new crop varieties with traits for enhanced nutrient and water use efficiency, weed suppression, and pest and disease resistance. The performance of these varieties in terms of crop yield and quality will be assessed under both management systems.

A contiguous block of five fields, covering 35 ha, has been set aside for the experimental platform. The rotation will include potatoes, winter wheat, two years of spring barley and beans. The conventional treatment will reflect current commercial practice. The sustainable treatment will include reduced herbicide and pesticide inputs, reduced tillage where appropriate and legume undersowing, compost additions and green manures to replace inorganic fertiliser applications. Both conventional and sustainable treatments will be flexible enough to track changes in commercial management practices and developments in sustainable technologies over time.

The general hypotheses are that 'sustainable' management, in combination with new crop varieties, will (i) maintain yield quality and yield stability at lower levels of agrochemical inputs, (ii) reduce greenhouse gas

(GHG) emissions and nutrient leaching from the system, and (iii) enhance soil quality and arable biodiversity. To test these hypotheses we will measure the responses of the whole system to sustainable management over a range of different crop varieties throughout each growing season over the course of at least four rotation cycles. Assessments will cover six main research areas: carbon and nutrient dynamics, soil biophysics, community dynamics, pest and pathogen populations, crop yield and quality, and field margin biodiversity. Trade-offs between these components of the system will be assessed through empirical and mathematical modelling.

The platform will provide a demonstration site for knowledge transfer, exchange and education activities, including specifically a resource for university undergraduate Honours and Masters projects. Three joint University of Dundee/SCRI PhD projects have already been proposed that are linked with the

Sustainability Research Platform and will make use of and contribute to the data generated. There is also a unique opportunity to engage with the UK farming community through LEAF. LEAF members will be given the opportunity to suggest novel management practices that they consider are likely to enhance environmental sustainability but are perhaps not sufficiently tried and tested for them to risk applying in a commercial situation. These practices can be incorporated into the sustainable treatment and their effects on crop production and the environment can be reported back to the LEAF membership via e-briefs, the LEAF newsletter, SCRI open days and Open Farm Sunday. Finally, the site will form part of a network of similar long term experimental platforms throughout Europe through the proposed FP7 Analysis and Experimentation on Ecosystems (ANAEE) design study, and through other EU funding opportunities including two further FP 7 collaborative projects currently in preparation.

Postgraduate studies at SCRI

Craig Simpson & Tracy Valentine

Postgraduate training at SCRI gives students the opportunity to study and investigate key questions in plant and environmental science, using state of the art equipment and to interact with staff who are at the forefront of their chosen disciplines. While we encourage coownership of their research areas with their supervisors, we support students by creating a research environment and use training programmes that promote personal development and stimulate the student's appreciation and understanding of their chosen area. On graduation we expect the majority of our students to be prepared to make a lasting contribution to the science base and

be responsive to worldwide changes and needs.

The University Joint Studentship Scheme continues to make an impact within the Institute, giving staff and students the opportunity to develop new and exciting areas of research within the framework of the science programmes. The success of this scheme has led to the largest presence of postgraduate students at SCRI for many years and they are impacting work in many ways across the Institute. The students are highly motivated, developing academically and technically demanding solutions to contemporary questions and problems.



Postgraduate students

The Joint Studentship Scheme further encourages Institute staff to form and establish strong interactions with universities across the UK, which allows development of research areas of value to SCRI.

On site we have further established quarterly meetings between PhD students and Institute staff. The aim of these meetings is to gain information and advice from senior experienced staff on topics and skills directly relevant to completion of a PhD and their future as a post-doc. Students on site have established a committee to discuss student matters directly related to them with the opportunity of bringing items before the University Interactions Committee (UIC) through two student representatives. Students are registered at universities throughout the UK, however, through our close partnership with the University of Dundee, post-graduate students working at SCRI can use the facilities available at the university, including English language tuition, training courses, library, scientific facilities and counselling.

This year sees the establishment of a new postgraduate team to administer, monitor and foster the considerable talents of SCRI students throughout their time at the Institute. We say goodbye to Gary Lyon as Institute Postgraduate Liaison Officer and David Marshall as chairman of the UIC and thank them both for their

support and development of postgraduate studies at SCRI.

PhDs awarded to students at SCRI

Comadran Trabal, Jordi. 2008. Association mapping of *Hordeum vulgare* in Mediterranean environments. University of Dundee PhD thesis.

Conner, Sean. 2007. Metabolomics as a tool to advance food safety: A model study using genetically modified potato. University of Dundee PhD thesis.

McLellan, Hazel. 2008. The involvement of Cathepsin B-like genes in disease resistance in *Arabidopsis thaliana*. University of Edinburgh PhD thesis.

Miller, Tim. 2007. Metabolite profiling of nematode–plant interactions. University of Dundee PhD thesis.

Mitchell, Carolyn. 2007. Novel approaches to the development of integrated pest management in UK raspberry production. University of Dundee PhD thesis.

Moleleki, Lucy. 2007. *Pectobacterium atrosepticum* effectors manipulate host plant defences. University of Dundee PhD thesis.

Morales-Osorio, Juan Gonzalo. 2008. Mechanisms of virulence and avirulence in the biotrophic interaction between potato and the late blight pathogen *Phytophthora infestans*. University of Dundee PhD thesis.

Ravensdale, Michael. 2008. A molecular study of the *cfI* and *cfa* gene cluster in *Pectobacterium atrosepticum*. University of Dundee PhD thesis.

Mylnefield Research Services Ltd

Nigel Kerby & Jonathan Snape

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

The Mission Statement of MRS is:

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

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

- spin out companies (for example, EnPrint Ltd)
- joint ventures (for example, Danasia Berry (Beijing) Corporation (Danasia) and Scottish Potato Technology Ltd (SPT))
- collaborative research projects (for example, long term breeding contracts with GlaxoSmithKline and Greenvale AP)
- licensing (for example, we have granted 473 licenses to plant varieties bred at SCRI)
- sale of products (for example, barley molecular markers, plant virus antibodies)
- analytical services (for example, stable isotope analysis, lipid analysis)
- field and glasshouse services (for example, supply of high-health plants, trialling new agrochemicals)
- consultancy (for example, statistical services from BioSS).

A core competence of MRS is the ability to assess these different routes to market for a particular technology, and develop and implement appropriate strategies.

Finances The turnover of MRS increased by more than 11% to reach £2.19 million in 2007/2008 which was in line with our budget and forecasts of our Business Plan. MRS transferred £1.2 million to the SCRI Group,

including £325k of Gift Aid. As in previous years, contract research (48%) was the biggest contributor to income, followed by royalties (26%) and lipid analysis (17%). The significant Gift Aid was largely due to royalty income from the raspberry variety Glen Lyon in Spain for the period 2006 to 2008. In addition, MRS retained £217k (after tax) to significantly increase company reserves for future investments.

Commercialisation Since its inception, MRS has always adopted a multi-faceted approach to commercialisation that encompasses the conventional patent and licence route as well as developing in-house analytical services (for example, Mylnefield Lipid Analysis, Stable Isotopes), spin-out companies (for example, EnPrint Ltd), joint ventures (Danasia, SPT). A key strand of our strategy is to develop new products, most notably plant varieties in collaboration with commercial partners, several of whom renewed long term breeding contracts in 2008.

EnPrint® EnPrint is a technology developed by Dr Tim Daniell for the rapid characterisation of complex populations of microorganisms. Following Scottish Enterprise Proof of Concept funding, MRS, together with Scottish Enterprise, funded further development of the technology. During this phase the technology was validated on samples provided by the Scottish Environment Protection Agency, marketing material was produced, including a website (www.enprint.co.uk), a trademark

was registered and a business plan written. At the time of writing, EnPrint Ltd has been incorporated and an investment of £150k in the business is in the final stages of negotiation.



David Rankin of Greenvale AP with Nigel Kerby and John Bradshaw

Licensing and IP asset management MRS places significant emphasis on the protection of IP generated by SCRI. Our IP portfolio is dominated by plant variety rights (45) but also includes three patents and six trademarks.

One of our key commercialisation routes is through licensing and we currently have 472 licences in 23 countries. Lesley Beaton is responsible for maintaining and enhancing the portfolio of plant variety rights, issuing trialling and testing agreements, granting licences, collecting royalties and arranging audits of propagators.

Since 1 January 2008, two potato varieties have been submitted to National List trials, three potato varieties have been added to the National List and four potato varieties granted EU Plant Variety Rights. In addition, EU Plant Variety Rights were applied for one raspberry variety. Big Ben, a new blackcurrant variety for the fresh market, was commercialised for the first time in 2008.

Vales Sovereign, a potato variety bred at SCRI in collaboration with Greenvale AP, was awarded the Tesco Fresh Produce Variety of the Year 2008.

Analytical services Mylnefield Lipid Analysis (MLA), under the leadership of Claire Traynor, had another successful year in 2008. Financial year 2007/2008 was the most successful ever with income exceeding

£378k. Due to this increased business activity, additional laboratory space was rented from SCRI and new equipment, including an HPLC and an auto-titrator was purchased. MLA was audited by the Medicine and Healthcare products Regulatory Agency (MHRA) twice in 2008 and is now able to analyse samples to Good Clinical Practice (GCP) and Good Laboratory Practice (GLP) standards if required by clients. An ongoing programme of staff training in these standards has been implemented. Lita Kelly joined Mylnefield Lipid Analysis in September 2008.

Dr Wolfram Meier-Augenstein, an internationally respected stable isotope chemist, joined SCRI in 2008. Following this appointment, MRS is able to extend the range of stable isotope analyses that can be offered. Lee Hunter continues to provide a commercial analytical service which was worth in excess of £80k in 2007/2008.

Developing markets MRS continues to make progress in developing new business opportunities in China. In 2008, Danasia, a cooperative Joint Venture with the Danish company Berryfine, a Chinese fruit growing and marketing company, Beijing Jinaodun and the IFU (a Danish government venture fund) was incorporated and issued a business licence. In return, for exclusive licensing of specific SCRI-bred soft fruit varieties, MRS will receive a 10% equity stake in Danasia. Seventeen tonnes of fresh fruit were sold in 2008 and over one million plants planted.

Knowledge transfer and exploitation MRS, on behalf of SCRI, is a partner in an Edinburgh based company, Genecom Ltd, which receives funding from EU and the UK Department of Innovation, Universities and Skills. This funding will be used to employ a new business development manager who will work alongside the existing MRS team in commercialising the intellectual property, expertise and resources of SCRI. In addition, SCRI is now eligible to apply for funding from the Genomia Seed Fund.

PhD studentships To demonstrate our long term commitment to plant breeding, MRS is funding a series of PhD studentships in field genetics. The first appointment is expected to join MRS in early 2009 and will



The Managing Director of MRS, Dr Nigel Kerby, greets the Chinese Minister of Agriculture, Mr Sun Zhengcai, at the official launch conference of the UK China Sustainable Agriculture Innovation Network (SAIN) in Beijing.

focus on potato breeding. In addition, MRS is the industrial partner in two CASE studentships. One is with Dr Ari Sadanandom of the University of Glasgow in the area of plant–pathogen interactions and the second with Professor Peter Urwin of the University of Leeds in the area of nematology. 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. David Walker, formerly Chairman of the British Potato Council, joined the MRS Board in April 2008 and brings an in depth knowledge of the UK and international potato markets.

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 Scottish Society for Crop Research

Bill Macfarlane Smith

The Society currently supports research on a range of topics, including research into novel resistance to Potato Virus Y2 in *Solanum phureja*; testing for virus resistance in raspberry; assessing the effect of changes in the Late Blight population on resistance of commercial cultivars, Commonwealth Potato Collection accessions and potential breeding material to the disease; and analyses of Institute weather records over the past 54 years for changes in the pattern of rainfall and other meteorological characteristics. Ongoing support is provided for the development of the Fruit Gateway website, and for the breeding of new raspberry cultivars through the Raspberry Breeding Consortium. Funding for a keynote speaker at the Crop Protection in Northern Britain Conference continues on a biennial basis.



Fruit for the Future, 2008.

The Annual General Meeting was held on 27th May 2008, and was followed by the Invited SSCR Lecture which was given by Professor Ian R Crute, Director of Rothamsted Research, whose subject was Science and the Land-based Industries in a Changing Environment.

SSCR is continuing its dialogue with the Office of the Scottish Regulator of Charities on the precise status of the Society. While there is no pressure on the Society to change from its existing Friendly Society status, no new such bodies are being brought into existence. The Society already complies with all the charity requirements on audit and the submission of its accounts to the Financial Services Authority, so it may well be that no changes are required to its existing position.

Knowledge Transfer continues to be a major interest of the Society and is achieved through the sponsorship and organisation of crop events, which are open to the general public as well as members, and half day technical meetings.

'Cereal Solutions', was held on 15 July 2008 at the Institute's Gourdie Farm and attracted 60 visitors. The demonstrations included plots of the Recommended List varieties of barley and wheat, genetic fingerprinting of barley, samples of barley bread and the use of wheat for distilling purposes. This will be the last such event under the current format as it will be replaced in 2009 by a joint SSCR/SCRI/SAC event to be entitled 'Cereals in Practice'. This will be held at the new SCRI farm at Balruddery on 7 July 2009.



Cereal Solutions, 2008.

The 'Fruit for the Future' event held on 17 July 2008 attracted 80 breeders, growers, end-users and processors. Existing Institute seminar room facilities are now inadequate to cater for the numbers attending and alternatives will have to be considered in future years. Research on raspberries, strawberries, blackcurrants and gooseberries was displayed, with prospective new varieties of raspberry available for tasting assessment. The occasion was used for the official launch of the new SCRI raspberry variety, Glen Fyne, by the Chief Executive and Director of SCRI, Professor Peter Gregory.

'Potatoes in Practice', held on 7 August 2008, continues to enjoy great support from the industry, with



Potatoes in Practice

well over 700 people in attendance. It is now the largest such outdoor event in the UK. Support is provided by the Potato Council, SAC, CSC Crop Protection Ltd., SCRI and the Society. Demonstrations on cultivars, agronomy and related research on pests and diseases of the crop continued to be major features, along with the steadily increasing demonstrations of potato crop machinery.

The Potato and Soft Fruit Crop Sub-committees held other half day meetings during the year to provide information on current research and interactions with processors and end users. The decision was taken to hold the Combinable and Energy Crops winter event at Battleby, on a biennial basis.

The Society's membership has now stabilised following a downturn over several years. A number of existing members have taken advantage of the recently introduced Life Membership category. The Committee of Management remains 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.

Publications

Publications listed between 1 October 2007 and 31 September 2008 are classified in the following manner:

- J Papers describing original research in refereed journals.
- R Books, 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)
- O Popular articles and unrefereed publications

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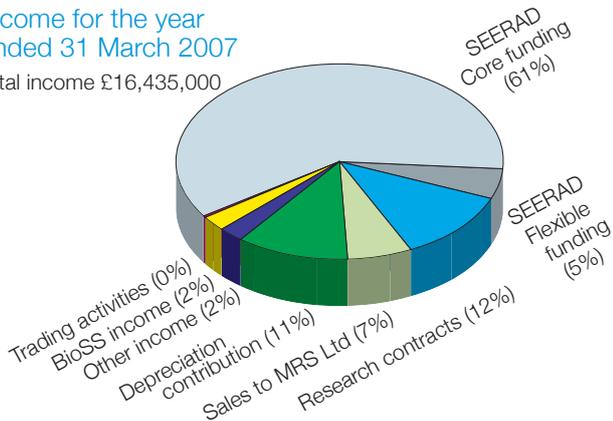
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Accounts

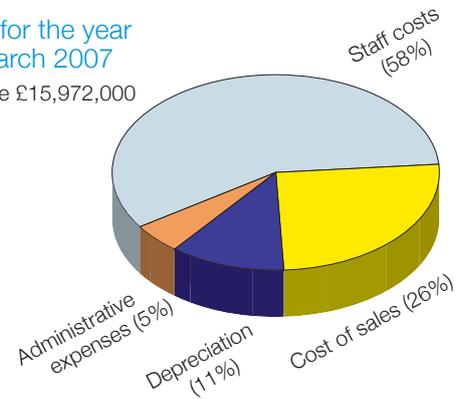
Income for the year ended 31 March 2007

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

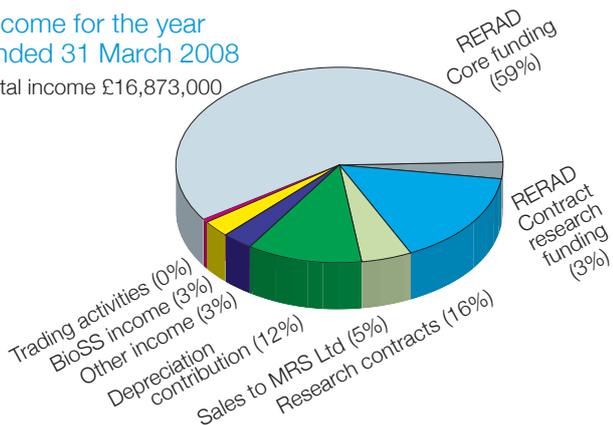
Fixed assets	94 %
Stocks	0 %
Debtors	6 %

Liabilities

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

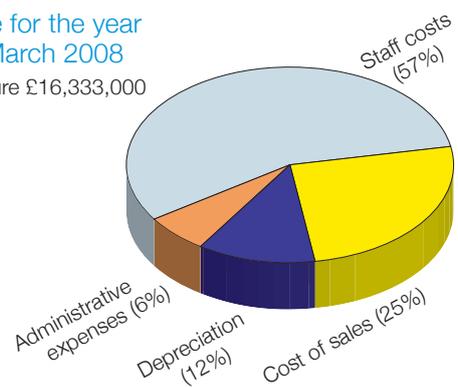
Income for the year ended 31 March 2008

Total income £16,873,000



Expenditure for the year ended 31 March 2008

Total expenditure £16,333,000



Balance sheet at 31 March 2008

Total value £35,204,000

Assets

Fixed assets	92 %
Stocks	0 %
Debtors	7 %

Liabilities

Capital reserve	82 %
Income & expenditure account	7 %
Current liabilities	11 %

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

Staff List

as at 1 October 2008

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^{4,12,13,14,15}

H V Davies BSc PhD CBiol FIBiol^{1,2,4}

D W Hopkins BSc PhD CBiol FIBiol^{16,17,20,21}

N G Hattersley BSc PhD ACMA



Genetics

R Waugh BSc PhD (Programme Leader)^{3,4}

J Alexander BSc

M M Bayer MSc PhD

N Bonar HNC

A Booth HNC

C Booth BSc

J E Bradshaw MA MSc PhD³

R M Brennan BSc PhD

G J Bryan BSc PhD

X Chen BSc PhD

G P Clark HNC BSc

J Comadran-Trabal BSc

M F B Dale BSc PhD³

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

C Hornyik BSc PhD

L Jorgensen HND

R Keith NEBS

D P King BSc

D Lewandowska BSc PhD

M S Liney HND

M E Looseley BSc MSc PhD

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

A Prashar BSc MSc PhD

G Ramsay BSc PhD³

L Ramsay BSc PhD

J Russell BSc PhD

P D Shaw MSc

C G Simpson BSc PhD

K Smith DipHE

P L Smith BSc

J Stephens BSc PhD

G E L Swan

J S Swanston BSc PhD CBiol MIBiol

W T B Thomas BSc PhD

A Weir

G Wilde

S L Williamson BSc

R N Wilson NCH

M R Woodhead BSc PhD

G R Young HNC

Mylnfield Research Services

D Coyle

D Clark

G Duncan BSc

L Ferguson

S N Jennings BSc



Plant Pathology

L Torrance BSc PhD (Programme Leader)³

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

P Cock MPhys MSc PhD

D E L Cooke BSc PhD

G H Cowan HNC MSc

A Dolan HNC

E Douglas BSc

B Fenton BSc PhD CBiol MIBiol³

G L Fraser

E Gilroy BSc PhD

D C Guy HND

N Holden BSc PhD

A M Holt

S N Humphris HNC BSc PhD

J T Jones BSc PhD³

S S Lamond

A K Lees BSc PhD

H Liu BSc MSc PhD

J Lynott BSc

S A MacFarlane BSc PhD

W J McGavin BSc

K D McGeachy HNC

H McLellan BSc

J McMillan

G L Malloch DCR BSc PhD

M Nasiadka

A C Newton BSc PhD

P F Palukaitis BSc PhD^{1,5,10}

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 PhD³

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 Taliansky PhD DSc¹¹

I K Toth BSc PhD⁶

R F Van Toor BSc PhD

E Warden ONC

S Whisson BSc PhD

N A Williams HNC

K M Wright MA PhD

V Young BSc

J Zhan BSc MSc PhD

A Ziegler BSc PhD

¹ Honorary Senior Lecturer in the University of Dundee

² Professor, Universities of Cordoba and Malaga

³ Honorary Lecturer, University of Dundee

⁴ Honorary Professor, University of Glasgow

⁵ Adjunct Professor, Cornell University

⁶ Honorary Lecturer, University of Aberdeen

⁷ Honorary Fellow, University of Edinburgh

⁸ Honorary Lecturer, University of Strathclyde

⁹ Honorary Professor, Heriot-Watt University, Edinburgh

¹⁰ Honorary Professor, Seoul Women's University

¹¹ Adjunct Professor, Moscow State University

¹² Visiting Professor, University of Reading

¹³ Honorary Professor, University of Dundee

¹⁴ Visiting Professor, University of Abertay, Dundee

¹⁵ Honorary Fellow, Rothamsted Research

¹⁶ Visiting Professor, University of Stirling

¹⁷ Adjunct Professor, University of Canterbury New Zealand

¹⁸ Special Professor, University of Nottingham

¹⁹ Visiting Associate Professor, Comenius University Bratislava

²⁰ Visiting Professor, Newcastle University

²¹ Honorary Senior Research Fellow, University of Glasgow



Plant Products and Food Quality

D Stewart BSc PhD (Programme Leader)
 C Cognat
 S C Conner BSc MSc CChem MRSC
 D Cullen BSc PhD
 H V Davies BSc PhD CBiol FIBiol^{1,2,4}
 G Dobson BSc PhD
 P M Dobson
 L J M Ducreux BSc MSc MPhil PhD
 R D Hancock BSc PhD
 R Hutchison
 H Kemp BSc PhD
 G J McDougall BSc PhD

D McRae ONC
 W Meier-Augenstein PhD CChem MRSC
 W L Morris BSc MSc PhD
 S D A Pont BSc
 J Rauscher
 H A Ross HNC PhD CBiol MIBiol
 L V T Shepherd BSc MSc PhD
 T Shepherd BSc PhD
 N Stewart BSc
 J A Sungurtas HND
 M A Taylor BSc PhD
 S R Verrall HNC

S Vivera BSc MSc
 P G Walker HND
 J F Wilkie
 Mylnefield Research Services
 W C Christie MBE BSc PhD DSc FRSE
 F Gunstone BSc PhD DSc FRSE
 L Hunter BSc
 L Kelly
 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)^{18,19}
 G Banks BSc MSc
 C Barnett
 G S Begg BSc PhD
 A G Bengough BSc PhD³
 K Binnie BSc
 A N E Birch BSc PhD CBiol MIBiol FRES³
 L K Brown BSc
 S Caul HNC
 T J Daniell BSc PhD²
 J Davidson BSc
 L Dupuy MSc PhD³
 R Dye
 F Falconer HNC

L Ford BA
 T S George BSc PhD
 D C Gordon HNC
 P D Hallett BSc PhD
 C Hawes BSc PhD
 D W Hopkins BSc PhD CBiol FIBiol
 R G Hunjan
 P P M Iannetta BSc PGCE(S) PhD
 S N Johnson BSc DPhil
 C Jorna
 A J Karley BA DPhil
 M Krol MSc
 S McClatchey
 B M McKenzie BSc PhD

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



University of Dundee, Division of Plant Sciences

J W S Brown BSc PhD^{3,4,13} (Head of Division)
 A Barakate BSc PhD
 P R J Birch BSc PhD (Principal Investigator)
 P Daly
 T Elaswed
 A J Flavell BSc PhD (Principal Investigator)
 J Grzebyta

C Halpin BSc MSc HDip PhD (Principal Investigator)
 S F Hubbard PhD (Principal Investigator)
 H G Jones MA PhD F1Hort (Principal Investigator)
 J Marshall BSc DPhil
 M Moragues
 K Rataj
 J A Raven BA PhD HonPhD(Umea) CBiol FIBiol FRS FRSE
 (Principal Investigator)

P G Schofield BSc PhD
 G G Simpson BSc PhD (Principal Investigator)
 L Spencer BSc
 N H Syed BSc PhD
 L Terzi BSc MSc PhD



Communication and Information Services

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

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

I R Pitkethly HND
 L Wakefield MA



Information Technology

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

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

V Pandey BSc
 P Smith BSc



Finance and Corporate Services

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

S Bell

A J Cartwright BA DMS MCIIPD

M Dalziel MA PgDPM MCIIPD

R G Davidson

M J De,Maine MBE BSc MPhil (Health and Safety Coordinator)

P Duncan

S Forsyth

K L Grant BA

B V Gunn

S Inglis

J Keith

C F Kydd FCCA

L Logie

A Pack BA

W Patterson HND

K Robb

A Sandilands

S Sinclair

M Soutar

E L Stewart

L Young



Engineering and Maintenance

S Petrie BSc (Head of Engineering and Maintenance)

J Anderson

D Byrne

C Conejo

G J E Ewart

A G Fox

D Gray HNC

K A Henry

R D McLean

I C McNaughton HNC

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

M Cook

A G Dobson HNC HND

I Fleming

J M Ford

A C Fuller

M A Grassie HNC BEd

P Heffell ONC

R Keith

M Lipska

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

A Ross HNC CPP

J B Snape MA MSc PhD CBiol MIBiol MBA

H Wilson HNC



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)^{8,9}

S M Bierman BSc MSc

A Butler BSc PhD

S Catterall BA MSc PhD

J M Dickson BSc

D Glancy

E M Heyburn MA

D Husmeier BSc PhD

G T Innocent

M A M Kirkwood DA

A D Mann BSc

G R Marion BSc MSc PhD

I J McKendrick BSc PhD

M Nath BSc MSc PhD

I M Nevison MA

D Nutter BSc

J Polechova BSc MSc PhD

A M I Roberts BSc MSc

J Sales BSc MSc

L Spezia BSc PhD

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

C A Hackett BA DipMathStats PhD (Acting Head of Group)

C Alexander BSc PhD

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	Name	Country of origin	Programme	Month/yr of arrival	Length of stay
A Aitken	UK	DU	May 08	2 mths	R McLeod	UK	PPFQ	Sep 08	1 wk
A Anderson	UK	DU	Jun 08	2 mths	A McNeill	Australia	EPI	Apr 08	2 mths
A Arshid	UK	PPFQ	Jul 08	1 wk	J Molman	Norway	PPFQ	Apr 08	1 mth
S Ashraf	UK	DU	Jul 08	2 mths	Q Molto	France	EPI / GEN	Jul 08	2 mths
M Bagavathiannan	India	EPI	May 08	1 mth	F C Nwoso	Nigeria	QHN	Jan 08	4 mths
G Bardin	France	PPFQ	Jul 08	2 mths	V Ord	UK	EPI	Jun 08	2 mths
C Barker	UK	PP	Sep 08	9 mths	E O-Rourke	UK	PP	Sep 08	8 mths
A Barton	UK	EPI	Sep 08	6 mths	A Oujj	Tunisia	DU	Aug 08	1 mth
J Biswas	India	EPI / BioSS	Jun 08	3 mths	M Ozcoban	Turkey	GEN	Jan 08	3 mths
F Bollenbeck	Germany	EPI	Apr 08	2 wks	P Panda	India	PP	Apr 08	6 mths
N Boukhelala	France	PPFQ	Jul 08	4 mths	K Paterson	UK	EPI	Apr 08	9 mths
S Bourgouin	France	GEN	Jun 08	2 mths	S Petitjean	France	EPI	Jun 08	2 mths
A Brehner	France	PP	Jul 08	2 mths	E Petrillo	Argentina	GEN / DU	Jun 08	1 mth
M Brown	UK	EPI	Sep 08	1 wk	A Pitman	UK	PP	Jan 08	1 mth
R Chawla	India	PPFQ	May 08	3 mths	N Potlandhurthi	India	PP	Apr 08	5 mths
Y-H Cheng	China	EPI	Jan 08	2 mths	A Pradelles	France	GEN	Jun 08	2 mths
H Clarke	UK	PP	Sep 08	9 mths	M Quader	Australia	PP	Mar 08	1 wk
M Cook	UK	GFS	Jan 08	2 mths	T Quinn	Ireland	EPI	Nov 07	3 mths
E Couchenay	France	EPI	Jan 08	1 mth	A R Raluca	Romania	GEN	Jan 08	2 mths
D Coyle	USA	EPI	Sep 08	2 wks	A Raymond	India	EPI	May 08	4 mths
T Csorba	Hungary	DU	May 08	2 mths	G Reed	UK	PPFQ	Oct 08	2 mths
S Deakin	UK	PPFQ	May 08	1 wk	A Rendall	UK	CIS	Jan 08	1 yr
M Destefanis	Italy	GEN	Sep 08	3 wks	A H Riepsamen	Australia	PP	Sep 08	4 mths
R Dhanalakota	India	PPFQ	May 08	4 mths	C Rizza	Italy	PP	Feb 08	6 mths
L Dou	China	DU	Sep 08	1 yr	C Rose	UK	EPI	Jun 08	2 mths
L Druva-Lustte	Latvia	EPI	Jan 08	1 mth	N Sapkota	Nepal	PP	Apr 08	4 mths
L Duncaff	UK	GEN	Jul 08	1 wk	T Sauras	Spain	EPI	Mar 08	6 mths
J Edgar	UK	EPI	Oct 07	5 mths	S Scibetta	Italy	PP	Jan 08	7 mths
T Elawed	UK	DU	Sep 08	10 mths	C Sebastian	India	PP	Apr 08	5 mths
F Ferguson	UK	FHR	Nov 07	1 yr	P Smtkal	Czech Republic	DU	Aug 08	1 mth
A Galbraith	UK	DU	Nov 07	4 mths	R Solomon -Blackburn	UK	PP / GEN	Oct 07	6 mths
S F Gatrell	UK	DU	Oct 08	5 mths	J Spencer	UK	PPFQ	May 08	1 mth
E Genet	France	QHN	Feb 08	7 mths	O Stasyk	Ukraine	DU	Feb 08	5 mths
A Gill	India	EPI	Jun 08	3 mths	C Steitner	Germany	GEN	Sep 08	1 mth
I Gordon	UK	DU	Sep 08	6 mths	R Stevenson	UK	DU	Oct 07	5 mths
C Gregory	UK	EPI	Jun 08	1 wk	C Streitner	Germany	GEN / DU	Aug 08	1 mth
A Hartmann	Germany	PPFQ	Sep 08	2 wks	A Summers	UK	GFS	May 08	1 mth
S Heinonen	Finland	PP	Jun 08	3 mths	B Sun	China	EPI	Aug 08	1 yr
R Hillis	UK	DU	Sep 08	6 mths	Y Tahira	Pakistan	PP / EPI	Jan 08	6 mths
K Hurt	UK	DU	Oct 08	5 mths	L R Tavares	Portugal	PPFQ	Aug 08	2 wks
B Levina	Latvia	DU	Sep 08	1 mth	F Taylor	UK	EPI	Jun 08	9 mths
C Imlay	UK	DU	Oct 08	5 mths	R Taylor	UK	PP	Apr 08	4 mths
E James	UK	EPI	Aug 08	1 yr	J Thomas	UK	IT	Sep 08	1 wk
L Jassogne	Australia	EPI	Apr 08	2 mths	C Todd	Australia	PP	Jul 08	1 mth
K Kampuss	Lithuania	GEN	Jan 08	1 mth	T Tsonev	Bulgaria	DU	Mar 08	3 mths
E N Kanichukattu	India	PPFQ	May 08	5 mths	M Vagiri	India	PPFQ	May 08	5 mths
S-H Kim	S Korea	GEN	Feb 08	2 wks	V Vasukuttan	India	PPFQ	May 08	5 mths
S Kubaytara	Syria	DU	Oct 08	5 mths	V Velikova	Bulgaria	DU	Mar 08	3 mths
N Kulkarni	India	QHN	Jan 08	3 mths	V Vendramin	Italy	GEN	Jul 08	3 mths
A Kumar	India	BioSS	Jun 08	4 mths	M Verrall	UK	EM	Jun 08	1 wk
S Kuwata	Japan	PP	Jul 08	3 mths	R Vetukuri	India	PP	Jan 08	7 mths
V A Laudicini	Italy	EPI	Jun 08	5 mths	S Vogel	Germany	PP	Apr 08	2 mths
S Laurent	Netherlands	GEN	May 08	4 mths	A Waseem	Pakistan	PPFQ	Oct 07	6 mths
J Lemaire	France	PP	Jul 08	5 mths	B Wentzel	South Africa	PPFQ	Feb 08	2 wks
I Lenclos	France	PPFQ	Jul 08	5 mths	T Wiechel	Australia	PP	Sep 08	1 wk
H Li	China	EPI	Jan 08	2 wks	J Ye	China	DU	Jun 08	2 mths
V Lund	UK	PPFQ	Jun 08	1 wk	F Yeo	Malaya	GEN	Mar 08	4 mths
S Manthri	UK	DU	Oct 08	1 yr	M Zamiatowska	Poland	EPI	Apr 08	8 mths
I Martinussen	Norway	PPFQ	Apr 08	1 mth					
T Mascia	Italy	PP	Apr 08	6 mths					
H McCulloch	UK	DU	Jan 08	2 mths					



Postgraduate students

Name	Programme	Project Title
Susan Breen	PP	Translocation of effector proteins into host plants.
Raymond Campbell	PPFQ	Genetics of carotenoid levels in potato tubers.
Emily Clark	EPI	Multitrophic factors influencing aphid vector competence in a spatially heterogenous environment.
Katy Clark	EPI	Does mother know best? Is host plant selection by above ground insects influenced by below ground herbivores.
Emma Coates	PPFQ	Anti-cancer effects of soft fruit phytochemicals.
Niki Cook	EPI	Population genetics of fernland sawflies.
Jayne Davis	EPI	Molecular interactions of potassium deficiency and pathogen resistance in barley.
Alexandre Foito	PPFQ	Development of metabolics based methods to benefit marker assisted breeding in perennial ryegrass.
Joanna Fyans	PP	The role of protein transport in the pathogenicity of <i>Streptomyces</i> spp.
Clement Gravouil	PP	Multiple disease interactions on cereals and interactions with other crop environment organisms.
Severine Grouffaud	PP	Translocation of <i>Phytophthora</i> effectors and their manipulation of host plant disease resistance.
Miriam Herold	EPI	Plant roots as drivers of denitrification.
Gerald Hochshartner	GEN	Application of a novel snoRNA marker system in plant evolution and systematics.
Ning Jiang	GEN	Linkage disequilibrium based mapping of complex traits in crops.
David Lloyd	GEN	Mapping genes and QTLs linked to flavour and texture in potatoes.
Kenneth Loades	EPI	Quantifying the role of fibrous roots on soil reinforcement.
Susan McCallum	GEN	Linking phenotype to genotype for fruit quality traits in raspberry.
Lindsay McMenemy	EPI	Cooperation between plant enemies – Do raspberry viruses attract more aphid vectors?
Katarzyna Rataj	GEN	Functional characterisation of the protein interaction domain of FPA.
Christelle Roberts	BIOSS	Prediction of promoter binding sites and transcriptional regulatory networks in two gamma-proteobacterial pathogen genomes.
Sonja Schmidt	EPI	Microtomography in soil root interactions.
Jane Shaw	PP	The role of Cajal bodies in the nucleolus in plant virus infection.
Nithya Subramanian	GEN	Increasing mineral delivery through potatoes.
Hui Tan	PP	Dissection of the Pectobacterium virulence quorum sensing regulation.
Amar Thirugnana Sambandam	PP	Role of seed-borne infection in <i>Rhychosporium</i> and <i>Ramularia</i> epidemics in barley.
Maja Thorsen	EPI	Biological mechanisms involved in stabilising sandy soils of the machair.
Stefanie Vink	EPI	Functional soil ecology and conservation in the machair in relation to changing land management.
Lea Weisel	EPI	Caesium uptake by roots of <i>Medicago</i> plants.
Tobias Wojciechowski	GEN	Root development in semi-dwarfing lines of wheat and barley.
Han Xiao	PPFQ	Function of polyphenols in chemoprevention.



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
Professor Claire Halpin BSc MSc H Dip 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
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(Umea) 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 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

SCRI Research Programme

ongoing as at 1 October 2008

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

RERAD Core – Programme 1

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

RERAD Contract Research Funding

SSCR/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.
SCR/919/07	<i>Dickeya dianthicola</i> – a threat to Scottish seed potatoes.
SCR/920/08	Sequencing the 'gene space' of potato chromosome 4, comparative analysis with tomato and development of a gene-based mapping platform.
BSS/845/06	Epidemiology, population, health and infectious disease control.

External research contracts

Agro-Transfert	Development of MAPP for the French market.
Biotechnology and Biological Sciences Research Council (BBSRC)	Visualisation and analysis of biological sequences, alignments and structures.
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.



Bioforsk	Systems experiments.
British Council	Analysis of the interaction between the pine wood nematode <i>Bursaphelenchus xylophilus</i> and the maritime pine <i>Pinus pinaster</i> .
British Ecological Society	Relationship between plant and soil microbial communities in different successional stages of <i>Abies pinsapo</i> Bioss. fir forests.
British Ecological Society	Sniffing out trouble: does the clay coloured weevil avoid leaves producing 'SOS' signals?
Chest, Heart & Stroke (via University of Dundee)	Cardiovascular function and intake of soft fruit: effect of qualitative and quantitative variation in berry antioxidant status.
Commercial	Brassica breeding.
Commercial	Soft fruit analysis.
Commercial	Potato breeding.
Commercial	Blackcurrant breeding.
Commercial	Lipid analysis.
Department for Environment Food and Rural Affairs (Defra)	Crop physiology.
Defra/HGCA	GREENGRAIN: Genetic reduction of energy use and emissions of nitrogen in cereal production (LINK).
Defra/RERAD	Integrated pest and disease management for high quality protected raspberry production.
Engineering and Physical Sciences Research Council (EPSRC)	Novel approaches to networks of interacting autonomes.
European Union (EU)	ALARM project.
EU	BIOEXPLOIT: Exploitation of natural plant biodiversity for the pesticide-free production of food.
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	SPICY: Smart tools for prediction and improvement of crop yield.
EU	Triticeae Genome: Genomics for <i>Triticeae</i> improvement.
EU Marie Curie	Role of arbuscular mycorrhizal fungi on the accumulation of radiocaesium by plants.
EU Marie Curie	Managing insecticide resistance in aphids in Scotland.
European Science Foundation	Exploiting genomics to understand plant–nematode interactions.
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.
French National Institute for Agricultural Research (INRA)	Global change at the microbial scale – effects of climate change on microbial decomposition and modulation of physical structure of soil.
Home-Grown Cereals Authority (HGCA)	BRIDGES: Breeding of wheat for resilience, improved distilling quality and greater environmental stability.

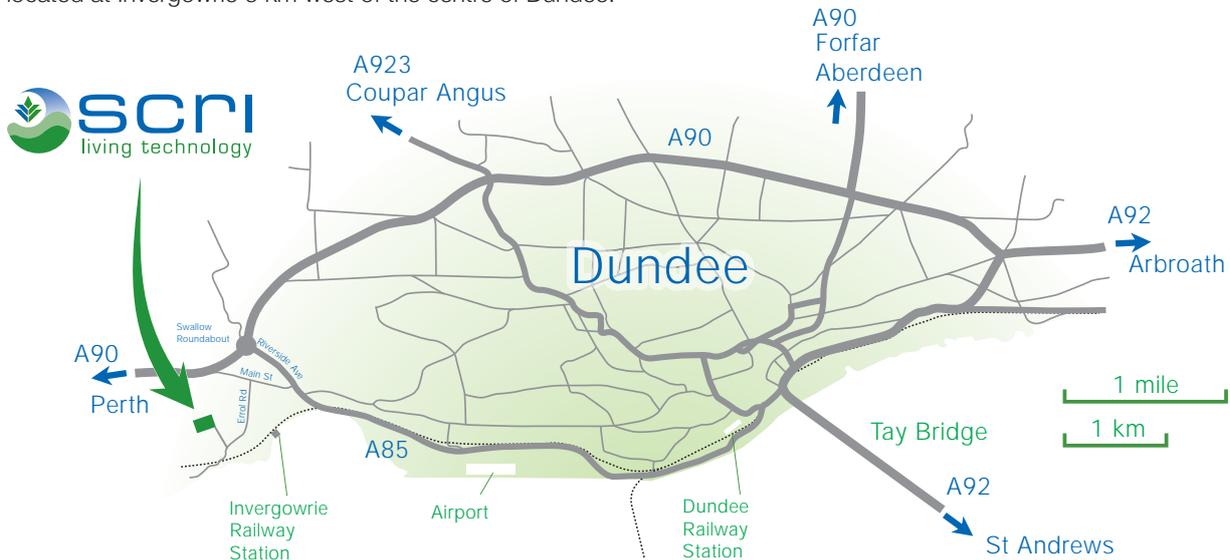
HGCA	Fungicide performance information for barley growers.
Horticultural Development Council (HDC)	Developing techniques to manage raspberry leaf and bud mite in tunnel produced raspberry.
HDC/RERAD/Commercial	The breeding and commercial development of new raspberry varieties.
International Atomic Energy Agency	Barley mutation grid.
International Maize and Wheat Improvement Center (CIMMYT)	Genomic dissection of tolerance to drought stress in wild barley.
Ministerio de Educacion y Ciencia (CICYT) in Spain	Study of the effect of the treatment with methyl jasmonate on the bioformation of chiral volatile compounds in vegetal foods.
Nairns	Knowledge transfer partnership.
Natural Environment Research Council (NERC)	Strategies to manage toxic cyanobacterial blooms in lakes: remote sensing, modelling and cost benefit analysis.
NERC (via University of Stirling)	Microbial diversity in Antarctic soils.
Potato Council	Survey of GB blight populations.
Potato Council	Review of umami in potato.
Potato Council	Independent variety trials.
Potato Council	Extending the scope of modern potato diagnostics and their interpretation.
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.
Royal Society of Edinburgh	RSE International Exchange Programme.
Rural Development Administration of Korea	Development of manipulation techniques of plant viruses for the development of multiple virus resistant horticultural crops.
RERAD/HDC	Developing a marker-assisted breeding toolkit for premium sensory characters in raspberries.
Scottish Enterprise	Additive-free treatments for shelf-life extension of minimally processed foods.
Scottish Enterprise	EnPrint.
Scottish Enterprise	Heath pea: development of a natural appetite suppressant.
Scottish Enterprise	Use of pathogen-derived inhibitors to delay plant senescence and to increase and widen plant transformation efficiency.
Scottish Enterprise	LEAF: Legumes for an energy efficient and environmentally friendly European agriculture.
Scottish Government	Reconnaissance survey of Irish potato in Malawi.
Scottish Funding Council (SFC)	Scottish Bioinformatics Research Network (SBRN) maximising bioinformatics infrastructure for Scottish Health, Agriculture and Industry.
Teagasc	Development of metabolomics based methods to benefit marker assisted breeding in perennial ryegrass.
Trans-Antarctic Association	Dry valleys ecosystem functioning.
University of Nottingham	Biofortification of wheat with selenium through agronomy and genotype selection to increase human dietary intake (LINK).
United States Department of Agriculture	Contribution to biological, virulence and molecular characterisation of <i>Globodera pallida</i> from Idaho.



Directions to SCRI

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

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



By road

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

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

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

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

By bus

Invergowrie is served by the 13,16 and 76 bus routes. There are bus stops on Main Street, Station Road and Errol Road and there is a footpath to SCRI between the houses on Errol Road. For information on travelling in Dundee visit the Dundee Travel Information website. For bus timetables and information see the Stagecoach Bus website.

www.dundeetravelinfo.com

www.stagecoachbus.com

By train

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

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). Flybe flies to Belfast City and Birmingham International airports from Dundee.

www.airfrance.co.uk

www.flybe.com

