Scottish Crop Research Institute

Annual Report 2004/2005

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The Scottish Crop Research Institute (SCRI) is a major international centre for research on agricultural, horticultural and industrial crops, and on the underlying processes common to all plants. It aims to increase knowledge of the basic biological sciences; to improve crop quality and utilisation by the application of conventional and molecular genetical techniques and novel agronomic practices; and to develop environmentally benign methods of protecting crops from depredations by pests, pathogens and weeds. A broad multidisciplinary approach to research is a special strength of the Institute, and the range of skills available from fundamental studies on genetics and physiology, through agronomy and pathology to glasshouse and field trials is unique within the UK research service.

Das SCRI ist ein führendes internationales Forschungszentrum für Nutzpflanzen im Acker- und Gartenbau sowie in der Industrie und auf dem Gebiet der allen Pflanzen zugrundeliegenden Prozesse. Es hat sich zum Ziel gesetzt, die Grundkenntnisse in den Biowissenschaften zu vertiefen; die Qualität und Nutzung der Kulturpflanzen durch die Anwendung konventioneller und molekular-genetischer Techniken und neuer agrarwissenschaftlicher Praktiken zu verbessern; sowie umweltfreundliche Methoden zum Schutz der Pflanzen gegen Verlust durch Schädlinge, Pathogene und Unkräuter zu entwickeln. Ein breiter multidisziplinärer Forschungsansatz ist eine besondere Stärke des Instituts; und das zur Verfügung stehende Spektrum an fachlichen Ausrichtungen, das von genetischer und physiologischer Grundlagenforschung über Agrarwissenschaften und Pathologie bis zu Gewächshaus- und Feldversuchen reicht, stellt ein einmaliges Forschungsangebot auf den Britischen Inseln dar.

Le SCRI est un centre international majeur de recherche sur les cultures agricoles, horticoles et industrielles et les processus fondamentaux communs à toutes les plantes. Son but est d'accrôitre les connaissances des sciences biologiques fondamentales; d'améliorer la qualité et l'utilisation des cultures par l'utilisation de techniques conventionelles et de génétique moléculaire et par l'application de procédés agronomiques nouveaux; de développer des méthodes de protection moins dommageables pour l'environnement contre les préjudices causés par les ravageurs, les pathogènes et les adventices. L'une des forces majeures de l'institut est une large approche multidisciplinaire de la recherche. L'éventail des techniques disponibles allant des études fondamentales en génétique et physiologie en passant par l'agronomie et la phytopathologie jusqu'aux essais en serres et aux champs est unique au sein du service de recherche du Royaume Uni.

Lo SCRI e' uno dei maggiori centri internazionali nel campo della ricerca sulle colture agricole, orticole e industriali e sui meccanismi fondamentali comuni a tutte le piante. L'Istituto ha come obiettivo principale l'accrescimento del livello di conoscenza delle scienze biologiche fondamentali, il miglioramento della qualità e del potenziale di utilizzo delle colture tramite l'applicazione di tecniche convenzionali o di genetica molecolare e di nuove pratiche agronomiche, lo sviluppo di metodi ecologici di protezione delle colture da agenti patogeni o malerbe. Uno dei punti di forza dell'Istituto e' l'adozione di un approccio largamente multidisciplinare (probabilmente senza eguali nel servizio di ricerca britannico) fondato su una vasta gamma di capacità scientifiche derivanti da ricerche di fisiologia e genetica ma anche di agronomica e fitopatologia supportate da prove di campo o in ambiente controllato.

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Introduction

P.J. Gregory

It is a great pleasure to introduce this Annual Report as the incoming Director. I began work at SCRI on 1 April 2005, following almost 25 years of pursuing a career at the University of Reading which was interrupted by about five years in Australia in the early 1990s. It is a delight to be part of a strong research institute that delivers excellent strategic research and simultaneously works in partnership with a range of commercial and public bodies to develop products and services of value to farmers, food processors, retailers and the general public. This unique combination of knowledge, products and services is a great testament to the work and foresight of my predecessor, Professor John Hillman, who retired after 19 years as Director on 31 March 2005. Many people conveyed their appreciation to John for all his efforts on their behalf over a prolonged period at the time of his retirement, but I should like to add my personal thanks to John for the excellent inheritance that I have received.

So, the period covered by this Report has seen change in the senior management, and many other changes will be evident throughout the body of the Report. First, and most obviously, I have made no attempt to emulate the thorough accounts of my predecessor about the state of agricultural research locally and globally, choosing instead to provide a brief statement of context for the Institute's work. Second, the period covered by the Annual Report has been changed from a financial year basis to the calendar year; this Report covers the changeover period so describes work conducted in the period 1 April 2004 to 1

October 2005. Third, following the approval of our Corporate Plan 2006-2011 by the Governing Body, we have restructured our senior management team to form a Senior Management Board, and reorganised our science into four programmes in which we believe we have realistic prospects of either sustaining or achieving excellence. Finally, and probably most importantly, 2005 has seen a great deal of staff time expended on developing ideas for research over the next five years that will contribute to the commissioned research programmes of our major funder, the Scottish Executive Environment and Rural Affairs Department (SEERAD). This change in the method of funding from block grant to commissioned research programmes heralds a new relationship between the Institute and SEERAD that follows directly from the revised approaches to supporting research outlined in "Strategic Research for SEERAD: Environment, Biology and Agriculture 2005-2010". The programmes, and their constitutive workpackages, provide a greater stimulus to scientists to work with members of other research institutes in Scotland to deliver the outcomes required and will, over time, lead to closer working relationships between research institutes and with universities.

Amidst this changing research and organisational landscape we have, however, continued to produce excellent new science of high impact, often in cooperation with other national and international partners. For example, the successful genome sequencing of the phytopathogen *Erwinia carotovora* (causing blackleg) and the identification of pathogenicity determinants released by the oomycete *Phytophthora infestans* (causing late blight) that are recognised by host defences, mark important steps in the Institute's research to develop potatoes resistant to these diseases. Similarly, phylogenetic analysis of accessions from the Commonwealth Potato Collection held at SCRI, together with accessions from the United States Potato Genebank, overturned previous hypotheses to support a single origin for cultivated potato located in the broad area of southern Peru.

Increasingly our research is related to government policy considerations, especially in relation to aspects of biodiversity on arable land. Research conducted as part of the field scale evaluations of genetically modified herbicide-tolerant (GMHT) maize showed that the forthcoming withdrawal of triazine herbicides would reduce, but not eliminate, the benefits for arable biodiversity of GMHT maize compared to conventionally managed maize crops. Our work to deliver healthy and nutritious foods to the public has also continued apace, with studies into the regulation and manipulation of carotenoid biosynthesis leading to better understanding of their metabolism in plants and realistic prospects for enhancing their content in potato.

We have also continued to develop new products in commercial partnerships mediated by Mylnefield Research Services Ltd. For example, in collaboration with one of our commercial partners, Greenvale AP, three new potato cultivars were nationally listed and protected by plant variety rights (Vales Sovereign, Vales Everest and Vales Emerald). Greenvale AP has high expectations of these varieties in the fresh and processing markets both in the UK and overseas. Mylnefield Lipid Analysis has expanded rapidly during 2005 to become the UK's leading independent laboratory for lipid analysis in food supplements, functional foods, blood samples for clinical trials and other pharmaceutical applications. Such partnerships are highly valued and, together with field days, exhibitions and talks to the land-based industries and the public, provide a rich network for knowledge exchange and transfer. These interactions benefit the Institute as well as many individuals and organisations.

This report highlights a small selection of our activities. I am delighted to be leading such a dynamic group of people and hope that you will enjoy reading about our activities.

Review of events – highlights

A key role for the Communications Office is organising a range of events to publicise new developments at SCRI, as well as producing publications to disseminate information about our research more widely. Visitors come from other research institutions to understand more about the role that SCRI plays in plant and environmental research, and special events are held regularly to inform food producers, processors and retailers, and the general public about our work and its outcomes.

School children in the Living Field Community Garden.

SCRI Open Day June 5th 2004.

Deputy Minister Allan Wilson opens the Glasshouse Complex at the SCRI Open Day June 4th 2004.

One of the most successful events of 2004 was the Open Day held on June 4th and 5th, when the general public were able to visit SCRI to see exhibits and demonstrations on many aspects of our research; the event was designed to be attractive to families, and the Deputy Minister for Rural Affairs took this opportunity to open the new glasshouse complex.

Fruit for the Future gives farmers, supermarket buyers and fruit processors the chance to taste raspberry selections that are in the fruit breeding process.

Other events are designed specifically for visitors from industry; these are organised collaboratively with the Scottish Society for Crop Research, Scottish Agricultural College (SAC) and the various levy boards. An example is 'Fruit for the Future', which showcases fruit research at SCRI, and previews the selections that will form the basis of new varieties. 'Cereal Solutions' focusses on our ongoing research on wheat and barley, including the Home Grown Cereals Authority (HGCA) funded research into wheat varieties suitable for animal and poultry feed, and distilling.

Cereal Solutions participants hear about the LINK project, GREEN grain.

'Potatoes in Practice' is now the premier field event of its kind in Scotland; sponsored by the British Potato Council (BPC) and organised by SCRI, SAC and CSC PotatoCare, the exhibition features a combination of field plots and marquee stands. This year's

Potatoes in Practice.

event attracted about 500 visitors, representing many sections of industry, government, and research organisations, as well as international delegations.

Opening the Living Field Community Garden, Jim McColl and Peter Gregory.

We also seek to focus on the new generation of potential scientists currently in education; this has encouraged us to find fresh perspectives for the presentation of our activities, and SCRI has had a visible presence during the year at science centres and school science fairs. A big ongoing success is 'The Living Field', which combines an interactive CD with onsite visits

School children enjoy the Living Field CD, an interactive tool designed to complement the school curriculum.

to SCRI's 'Community Garden'. A highlight of the year was the opening of the Garden by Jim McColl, presenter of 'Beechgrove Garden'; this took place on 17 August 2005, and was attended by 110 school children. Other visitors on the day included education advisers, science centre staff, local politicians, and many others who had provided input to the project. The event was extensively covered by the press who highlighted SCRI's unique role in educating Scottish children about their environment.

The Living Field CD.

The influence of SCRI's scientific research extends far beyond Scotland. Visiting scientists, politicians and farmers all add to the exchange of information and participate in the process of knowledge transfer. Recent visits have included a delegation from the National Natural Science Foundation of China (NSFC), which was headed by the European Director for the Bureau of International Cooperation; the purpose of their visit was to discuss ways of improving food quality by biochemical methods. Senior members from the provincial government of Sichuan also visited, forging encouraging links for future cooperative work.

Nigel Kerby and Finlay Dale host a delegation from the Chinese province of Sichuan.

Professor John Hillman's retirement

Professor John Hillman retired on 31st March 2005 after 19 years as Director of SCRI. John was appointed as Director at SCRI in March 1986, bringing with him a wealth of experience and achievement in the world of biological research. Many present and retired staff attended the party organised to mark his retirement at which a portrait, commissioned to hang in the Boardroom, was unveiled. Howard Davies presented him with gifts and messages of appreciation for his outstanding service to the Institute.

Born in Kent, John was educated at University College, Aberystwyth, obtaining a First Class Honours degree in Botany in 1965 and a PhD in Plant Physiology and Biochemistry three years later. His first appointment was in the University of Nottingham, School of Agriculture, then from 1971 to 1986 he was first a Lecturer, then Senior Lecturer, Reader, and finally Professor and Head of the Department of Botany in the University of Glasgow.

During his time at SCRI, John won many awards for his achievements including an Honorary DSc University of Strathclyde 1994; Honorary DSc University of Abertay Dundee 1996; British Potato Industry Award 1999; International Potato Industry Award 2000; Dr Hardie Memorial Award 2001; and Scottish Horticultural Medal 2003.

John lectured widely, both in the UK and abroad, and, despite the many demands on his time, has managed

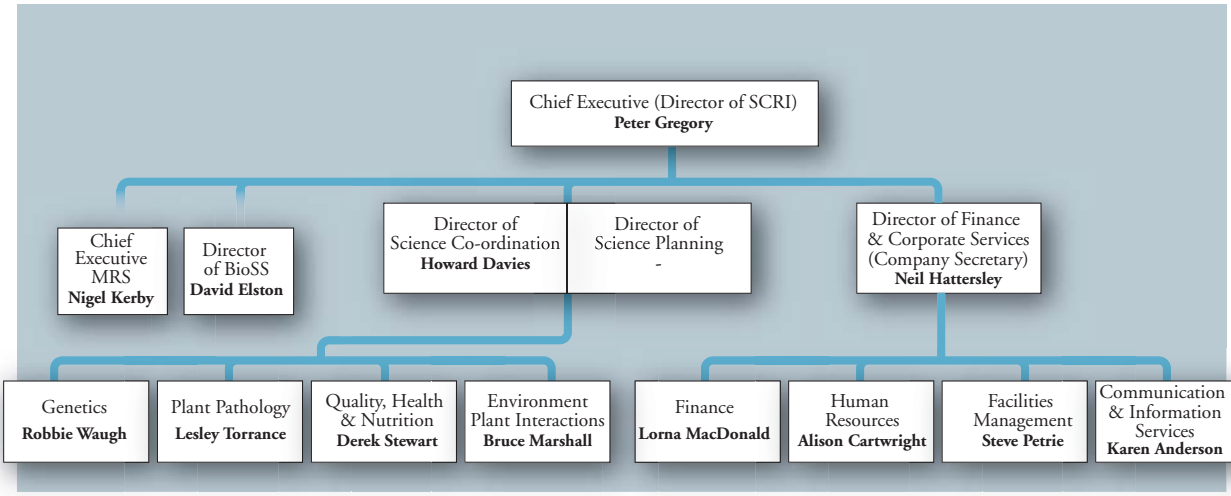
to maintain his research interests and involvement, covering a wide range of topics from plant growth regulators, through carbon metabolism to gene banks and genetically modified crops. To all of these activities, he brought an unrivalled breadth of knowledge and wisdom. John was a staunch defender and campaigner on behalf of SCRI. He has also fought vigorously on behalf of the agriculture, horticulture and biotechnology industries.

As Professor Howard Davies made the presentation he said "Successful Institute Directors are visionaries and tenacious supporters of the highest quality of research possible. Prof. Hillman has undoubtedly proven himself at the highest possible level, transforming SCRI into a truly international research centre which can be proud of its achievements".

Organisational Structure

H.V. Davies

In the last annual report the science management structure of SCRI consisted of a Director, Deputy Director three Theme co-ordinators and nine Programme leaders. With the commissioning by SEERAD (from April 2006) of science Programme Area 1 'Profitable and Sustainable Agriculture-Plants' (co-ordinated by SCRI) the Institute has implemented structural changes which will ensure delivery of the commissioned research and which also flags its strategic intent to evolve its science base to provide contemporary solutions in areas of science relevant to modern crop production systems within appropriate ecological frameworks. Programme Area 1 consists of six Workpackages driven by individual Workpackage Leaders. The Workpackages are: Potato Genetics, Potato Pathology, Barley Genetics, Barley Pathology, Soft Fruit Genetics & Pathology and Sustainable Crop Systems. SCRI has also identified the need for broader integration of research activities and resource management across Workpackages and has therefore developed, for its own purposes, four Programmes driven by Programme Leaders to fulfill these objectives. The Programmes are Genetics, Pathology, Quality Health & Nutrition and Environment Plant Interactions and represent areas of science in which SCRI has known strengths. The Director of Science Co-ordination has a major primary role in ensuring delivery on SEERAD and externally funded research and the Director of Science Planning (appointment in progress) will implement strategies for evolving the Institute's science focus and cross-disciplinarity. These, together with the Director of Finance and Corporate Services, will report directly to the Chief Executive, Prof. Peter Gregory.



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Genetics

R.Waugh

A new Director, allied with new external political, social and environmental agendas, have prompted a shift in organisational focus and change in our operational structures. 'Genetics' has emerged from the amalgamation of components of three previous research groupings (Genome Dynamics, Gene Expression and Computational Biology) and will build on areas of established scientific excellence to address some of the new and challenging objectives facing the plant research community today. Without doubt this will require changes to our previous activities, particularly as opportunities emerge to investigate, amongst other things, non-food uses of crops, resource use efficiencies, plant development and environmental impact. Our future work will re-emphasise the need for greater innovation and basic research in plant science, a view consistent with the development of a vigorous, world leading bio-based economy in the UK over the next 20 years. Our vision is that a strong basic research portfolio that continually provides ideas and discoveries will fuel cycles of translation and exploitation in applied-basic genetic programmes. The need to strengthen the links between discovery and application will be a major driver.

The principal challenge of the Genetics Programme is to relate variation at the level of the gene and genome to variation in characteristics which are relevant to end user needs. Appropriate germplasm is therefore essential and access to well characterised and well maintained bio-diverse plant collections underpin all aspects of the research programme. We will continue to use pre-breeding as the primary mechanism for delivering our research outputs to the user community. The Genetics Programme research is organised into five overlapping themes.

Genome Biology The genetic dissection of important traits and identification of the underlying genes requires that resources and strategies be developed to enable large-scale investigations across whole genomes or targeted genome segments. Powerful enabling technologies, such as high throughput molecular markers, expression arrays and mutant populations developed at SCRI and elsewhere, will facilitate this process and their exploitation will be central to our future objectives. To facilitate gene isolation we will contribute to global initiatives to develop genetically anchored physical maps of all of our established crop groups (barley, potatoes and *Rubus*). We have participated in the development of a unified international vision and roadmap towards obtaining full genome sequences of wheat and barley that has been articulated by both the European Triticeae Genomics Initiative (ETGI) and In-

ternational Triticeae Mapping Initiative (ITMI). The vision recognises the enormity of this task and supports a staged process involving additive contributions from multi-national efforts. Our current contribution involves linking the emerging physical map with the genetic map. We are similarly involved in the international potato genome sequencing consortium (PGSC) that aims to sequence the entire potato genome and with the Rosaceae genome project that will exploit our large insert raspberry DNA library for comparative genetics. These efforts rely on the development of genetically anchored physical maps, and genetic markers and technologies that we have developed are playing a central role in each of these projects.

Genetics and Breeding Translating discoveries from applied-basic research into tangible deliverables that have commercial or societal impact will continue to be a key area of our future endeavours. We will focus on identifying the location of genes underlying traits that are of environmental, commercial and consumer importance. In potatoes these include taste, texture and resistance to the golden potato cyst nematode (PCN) and late blight pathogens. In barley, yield, quality and end-use characteristics remain the major foci while in soft fruits the major industry requirement for health associated characteristics and resistance to the pests and pathogens that have the potential to devastate the industry are our highest priorities. We will begin to apply modern genetical approaches such as association genetics to enhance our ability to identify the genetic locations of the genes controlling these characters. Exploiting the acquired genetic knowledge will be achieved by deploying genetic or phenotypic markers to mobilise these desirable characteristics into adapted or elite germplasm which we anticipate will be embraced by our commercial partners in their bespoke crop improvement programmes. As an example, PCN is the biggest threat to the potato industry in the UK. We are currently mobilising several sources of resistance to PCN, that we identified by screening exotic potato germplasm from the Commonwealth Potato Collection (CPC), into UK adapted material. In addition to these practical outputs, the process of genetic discovery provides the genetic materials required for gene isolation and validation. The outputs from this research will be our primary point of interaction with commercial partners, levy boards and Government departments.

Genes and Development Identifying the genes involved in biochemical, molecular or developmental processes is the first stage in understanding and dissecting genetic pathways and molecular interactions

that form the basis of complex phenotypes. Enhanced by the presence of three University of Dundee groups, we are extending our investigations into basic biological processes that underpin aspects of plant development, growth and response to environmental stimuli. For example, flowering time in plants is sensitive to ambient temperature, and phenology data provides some of the most compelling data for global warming. However, almost nothing is known of how ambient temperature is perceived and signalled to control flowering and investigating this issue is directly relevant to understanding and predicting the potential impacts of climate change. From a practical point of view, developing earlier flowering varieties, or varieties with more rapidly maturing grain will potentially address optimal production requirements for the Scottish environment. Understanding regulatory networks and biochemical pathways will be required for the development of new and desirable phenotypes through a combination of both genetic and GM approaches.

Biodiversity Crop plants have evolved from their wild ancestors by the processes of domestication and subsequent selective breeding over the last *ca.* 10,000 years. As a result, only a fraction of the total number of allelic variants present in the wild progenitors has contributed to the present day cultivated gene pool. However, wild germplasm harbours an unknown quantity of potentially valuable alleles that have been inadvertently excluded from current elite lines. Indeed, many studies have demonstrated the value of alleles originating from wild and locally adapted germplasm. One of our major challenges is to explore and understand plant biodiversity in natural and agricultural systems. Our goal is to gain detailed knowledge of patterns of genetic diversity within a species to identify potentially useful alleles either for importation into breeding programmes or to inform conservation policy. We are particularly interested in genes implicated in traits deemed essential for sustainable and environmentally sensitive crop production in the face of climate change. We are combining high throughput genomics approaches with traditional skills in genetics and phenotyping to clarify the relationships between existing groups of species, to explore the link between sequence variation, recombination and linkage disequilibrium, and to quantify biological diversity of native and endangered species for conservation purposes.

Bio-informatics, Biomathematics and Statistics Computational biology is a key component of all contemporary biological research programmes and a mechanism to pursue innovative new research in its own right. Good informatics capabilities are necessary to archive, manipulate, analyse and display the unprecedented amount of data that can be generated in a modern research programme and to exploit the freely accessible data present in the public domain. We have already established a number of web-accessible databases that provide a public face to much of the data and resources generated within the research programme and are extending our research capability in this area by integrating locally produced information with relevant data from other sources. This is particularly relevant to exploiting comparative information from model organisms which can provide a template for our work on crops. To tie in with our crop specific genetics programmes we are extending our studies on linkage disequilibrium in inbreeding and outbreeding species, comparative genome and sequence analysis, ontology and annotation and analysis of metabolic and regulatory pathways. We anticipate that this will be an area of continuing growth.

Three University of Dundee groups are fully embedded in the Genetics Programme and they significantly enhance our research activities. In particular, the Genes and Development research theme benefits from internationally recognised research on lignin biochemistry and genetics (C. Halpin) and on the control of flowering (G.G. Simpson), and the Biodiversity theme by research on plant genome diversity and evolution (A.J. Flavell). These groups provide great scope for interaction and synergy and a number of collaborative research projects have already been established within the Programme.

It is an exciting time to be involved in plant science and I consider that the quality of research currently being carried out within SCRI has never been higher. This has been recognised and rewarded recently by the successful acquisition of a substantial amount of competitive funding from a range of sources which will support and extend our research. A few highlights of the year, which cut across the five research themes outlined above, are presented in the following articles by P.E. Hedley *et al.* and G.J. Bryan *et al.*

A single domestication for cultivated potato

G.J. Bryan, K. McLean, R. Waugh, D. Spooner[a] & G. Ramsay

The potato has been grown as a native food crop in South America for over 7000 years. First introduced to the UK as a curiosity in the late 16th century, the potato rose to its current position as a staple food following its adaptation to local conditions in the late 17th century. The precise origins of the humble potato, intimately linked with the pre-Inca civilisations of the central Andes, have always been enigmatic. We have recently been engaged in some work that has shed significant light on the evolutionary origins of the cultivated potato. Potato is part of the plant genus *Solanum*, an extremely diverse group of flowering plants containing over 1500 species. Over 200 tuber-bearing potato species have been described, including the common cultivated tetraploid potato, *Solanum tuberosum* ssp. *tuberosum*, and a small number of other primitive cultivated species. These other types include the tetraploid *S. tuberosum* ssp. *andigena*, the primitive form of the European potato, as well as *S. phureja*, a diploid species which is now being used in UK breeding programmes, as typified by the varieties Mayan Gold and Inca Sun.

Our study is based on the use of 450 Amplified Fragment Length Polymorphism (AFLP) markers on a large collection of potato germplasm known as the Commonwealth Potato Collection (CPC), which is maintained at SCRI. In 2001 we embarked on a groundbreaking study to obtain the genetic fingerprints of all 1500 'accessions' in the CPC, as part of a project to elucidate the evolutionary relationships of potato species, and perhaps more importantly, to allow us to make better future use of the CPC in potato breeding. AFLP markers were chosen because of their high level of reliability and their high multiplex ratio, whereby a single primer combination can yield 50-100 scoreable markers. AFLPs represent an extremely efficient method for generating DNA-based marker fingerprints for plants representing genebank accessions. Moreover, AFLPs have been shown to be suitable for the phylogenetic analysis of diverse potato germplasm[1]. The AFLP marker data set we have generated is one of the largest ever generated for a plant germplasm collection and presents significant oppor-

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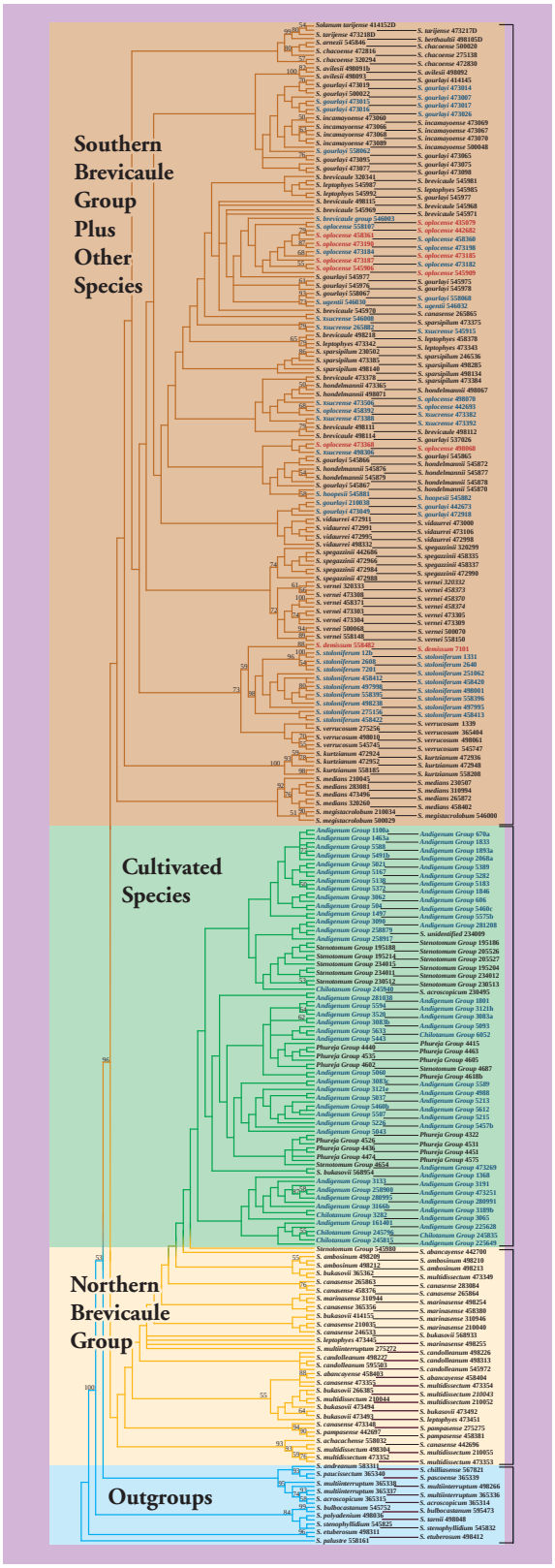

Figure 1 A simplified phylogenetic tree containing 264 wild (including 3 outgroup accessions) and 98 cultivated accessions of potato.

tunities for the improvement of knowledge concerning the taxonomy of the over 150 wild and cultivated potato species included in the study. To facilitate analysis the data set has been partitioned into smaller data sets designed to examine particular questions. One of these relates to the evolutionary history of the various species of cultivated potato, the most well-known of which is the common potato *S. tuberosum* ssp. *tuberosum*. The potato has been cultivated for thousands of years, but there has been a great deal of scientific debate about its origins. Our study was designed to assess whether the domestic potato arose from a single wild progenitor or whether it arose multiple times from species distributed across the whole length of Southern America. Most evolutionary hypotheses have centred around a group of about 20 morphologically very similar tuber-bearing wild species, referred to as the *S. brevicaule* complex, distributed from central Peru to northern Argentina. In order to address this question we have performed a phylogenetic analysis of an AFLP marker data set from 264 wild and 98 cultivated potato accessions. The phylogenetic tree, reprinted in simplified form from a recent publication[2], resulting from this analysis is shown in Fig. 1. This tree is concordant with previous trees based on use of morphological and other types of marker data in suggesting a clear 'northern' and 'southern' split for the members of the *S. brevicaule* complex. These data are also suggestive of the need for a reduction in the number of species in the complex. The most significant result from this analysis is the observation that, in contrast to many prior hypotheses of multiple geographically-diverse origins of the cultivated potato, a single origin from a broad area of southern Peru has been identified. The 'multiple-origins' theory was based in part on the broad distribution of potatoes from north to south across many different habitats, through morphological resemblance of different wild species to cultivated species, and through other types of data. Our data are unequivocal in suggesting a single domestication from the 'Northern' component of the *S. brevicaule* complex.

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Epiheterodendrin in malting barley: molecular evidence for cytochrome P450-mediated production

P.E. Hedley, I. Hein, A. Booth, S. Williamson, J. Morris & J.R. Russell

Cyanogenesis in barley: a quality problem for the Scotch Whisky industry. Many plant species produce cyanogenic glucosides which, through release of the breakdown product hydrogen cyanide (HCN), have been implicated in the natural defence response to herbivores and pathogens, and are also believed to have roles in nitrogen storage and osmoregulation. In certain cultivars of barley, known as 'producers', a leucine-derived cyanogenic glucoside, epiheterodendrin (EPH), is present at high levels in young seedlings (malt). Fermentation of malted barley leads to hydrolysis of EPH, via action of yeast-derived β-glucosidase and subsequent heating during distillation, to form HCN. A reaction within the distillate between HCN and ethanol, in the presence of copper and oxygen, leads to trace but significant levels of the potentially carcinogenic compound ethyl carbamate. Low ethyl carbamate varieties of barley are therefore high priority for the Scotch Whisky industry, leading to our detailed molecular characterisation of EPH pathways and development of an unambiguous marker for varietal selection by malting barley breeders.

Characterisation of EPH genes from barley Cytochrome P450 enzymes form the largest family of plant proteins, with over one thousand members identified, catalysing a wide array of both simple and complex reactions, generating a diverse range of natural plant products. EPH has been proposed to be derived from the amino acid leucine through action of two cytochrome P450 enzymes, cyp79 and cyp71. Barley ESTs with homologies to cyp79 and cyp71 were identified, representing partial 3' cDNA sequences, and the corresponding gene fragments were

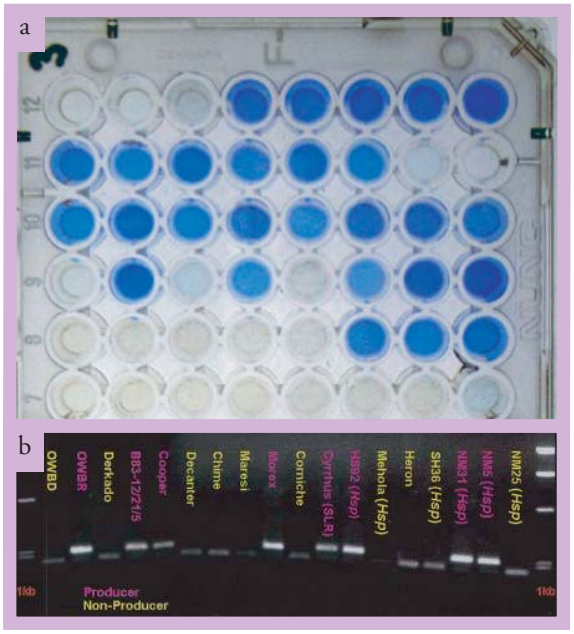
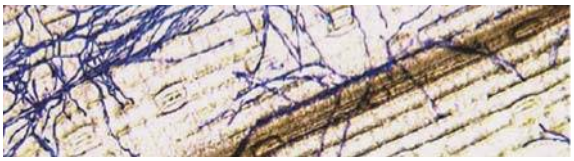


Figure 1 (a). Phenotypic assay of EPH activity: clear represents 'non-producers' and blue represents 'producers'; (b), Genotypic determination using multiplex PCR-based screen: 'producers' are in red and 'non-producers' are in yellow.

subsequently isolated using PCR. These gene probes were used to screen a barley (cv. Morex) bacterial artificial chromosome (BAC) library to isolate the full-length gene sequences. Fingerprinting of the BAC clones, utilising SNaP-shot-based fluorescent labelling of restriction-digested fragments, clustered the clones into two distinct groups. Single BAC clones for each gene were subcloned and sequenced revealing full length genes encoding cyp79 and cyp71, which contain two and three exons respectively, and also indicate the presence of putative retroelement sequences, which are a common feature of the barley genome. Expression of *cyp79* and *cyp71* genes were determined by real-time PCR, and both genes were clearly up-regulated in EPH 'producers' compared to 'non-producers' and showed similar patterns of temporal decrease in expression levels between 3-day and 4-day-old seedling leaf material. Using polymorphic barley populations, both genes genetically mapped to the same position, which was also confirmed as the EPH locus on chromosome 1H, first identified at SCRI.

Development of an EPH molecular marker Central to selection of barley varieties with low levels of potential ethyl carbamate generation is the development of a robust unambiguous molecular marker. Previously at SCRI, a simple-sequence repeat (SSR) marker (BMAC213) was generated which showed good, but not complete, association with the EPH phenotype, as determined by the biochemical assay. Oligonucleotide primers were designed to re-amplify regions of the *cyp79* and *cyp71* genes in a range of 'producer' and 'non-producer' barley accessions, including cultivated, landrace and wild barley germplasm. These primers only amplified in the 'producer' accessions, the *cyp79* gene product being absent in 'non-producers'. This complete association with the EPH phenotype, clearly distinguishing 'producers' from 'non-producers', was therefore used as the basis for development of a multiplex PCR-based screen (Fig. 1). This assay is currently being used for efficient, reliable and cost-effective marker-assisted varietal selection in commercial malting barley breeding programmes.

Acknowledgements
Special thanks to Wayne Powell (NIAB), Stuart Swanston, Bill Thomas and James Brosnan (SWRI) for useful discussions.



Plant Pathology

L. Torrance

Changes in the organisation and management structure of SCRI during 2005 have resulted in the formation of a new Plant Pathology Programme to investigate economically important pests and pathogens. The research covers a range of scales from the molecular and cellular to that of pest and pathogen populations. The overall aims are to understand disease processes and provide knowledge and strategies for crop improvement through durable resistance and sustainable disease control strategies. Much of the work is geared to improvement of potato, barley and soft fruit.

There are three major areas of research:

Plant response to pathogens To understand the cell and molecular mechanisms of disease resistance and susceptibility, to provide underpinning knowledge for durable disease resistance.

Pathogen genomics To conduct whole genome sequencing and comparative genomics to provide knowledge of effectors, mechanisms underlying pathogenicity, horizontal gene transfer and intraspecific variation.

Pest and Disease Management To understand mechanisms of pest and pathogen transmission, disease development and factors driving population change and evolution, to develop sustainable control strategies.

The programme has close links to the Genetics and Plant Environment Interactions programmes particularly through research on pest and disease resistance and survival of pathogens in managed ecosystems and we expect to develop and strengthen these links in future e.g. through the work described below on *Erwinia*.

Research highlights during the year include:

An unusual structure at one end of potato potyvirus particles Potyviruses are transmitted by aphids in a non-persistent manner and can spread readily in crops during the growing season; they have filamentous particles that are generally supposed to be assembled from many copies of a single type of coat protein. Using atomic force microscopy and immunogold labelling techniques we have demonstrated that filamentous helically-constructed particles of potyviruses, *Potato virus Y* and *Potato virus A* contain a novel and unusual structure at the virion end containing the 5'-end of the RNA. Such a structure contains virus-encoded proteins, VPg and helper component proteinase, and potentially plays key roles in different virus-encoded functions such as virus assembly/disassembly, movement and vector transmission (published in *Journal of Molecular Biology*).

A novel role of the nucleolar protein fibrillarin in plant virus systemic infection For many years, plant RNA-containing viruses were thought to replicate and assemble mainly in the cytoplasm of cells, but recently we have shown that a number of plant viral proteins such as the long-distance movement (ORF3) protein of *Groundnut rosette virus* (GRV), an umbravirus, enter the cell nucleus, and specifically target the nucleolus. These findings led us to propose the existence of a novel nucleolar function associated with regulation of plant macromolecular transport via the phloem, the long-distance transport system for the products of photosynthesis and nitrogen metabolism in plants. The mechanism of nucleolar involvement in the long-distance transport was elucidated: we found that the nucleolar protein fibrillarin is targeted by the viral ORF3 protein and relocated to the cytoplasm where it mediates assembly of transport-competent complexes containing viral RNA which then move through the phloem.

New role for virus triple gene block (TGB) movement proteins Intracellular localisations of fluorescent protein-tagged triple gene block (TGB) movement proteins of *Potato mop-top virus* (PMTV) and *Barley stripe mosaic virus* (BSMV) were examined by confocal laser scanning microscopy of living cells. We found differences in subcellular distribution of the TGB2 of the two different viruses which indicate subtle differences in the role and function of these proteins in virus movement. Moreover, we have revealed for the first time that the TGB2 of PMTV and the cysteine rich γb protein of BSMV play roles in establishing replication complexes in chloroplasts.

Virally-expressed cDNA libraries provide novel protein localisations In a project funded by The Gatsby Foundation, we have successfully constructed virally-expressed cDNA-GFP fusion libraries from *Arabidopsis* and *Nicotiana* sp., and used them to search for proteins that localise to different subcellular structures. In the last year, many novel proteins have been discovered. The data has been uploaded to ProtLocDB, a web-enabled database (http://bioinf.scri.ac.uk/cgi-bin/ProtLocDB/home), which is publicly available and has been accessed by a number of labs worldwide.

Origin of siRNAs in response to virus infection in plants is described in the following article by C. Lacomme *et al.* (published in *Journal of Virology*).

VIGS-based functional characterization of genes associated with powdery mildew resistance in barley (see following article by C. Lacomme *et al.*).

Survival of *Erwinia carotovora* in managed systems Studies of the complete genome sequence of the

potato blackleg pathogen *Erwinia carotovora* susbp. *atroseptica* (*Erwinia*) have led to the discovery of a binding protein delivered by a Type I secretion system that appears to be responsible for binding of *Erwinia* to the roots of brassica plants but plays no part in binding to potato roots. The presence of other genes (within the *Erwinia* genome sequence) that are often associated with root-dwelling organisms and which code for traits such as the ability to fix nitrogen, the breakdown of root exudates and the production of competition-reducing antibiotics further supports this hypothesis. Work is in progress to investigate whether such alternative hosts aid *Erwinia* survival in managed ecosystems for the subsequent contamination of high grade seed potatoes.

The first *Phytophthora infestans* avirulence gene As part of an international collaboration, the first avirulence gene, *Avr3a*, has been isolated from the late blight pathogen, *P. infestans*, which encodes a protein that is recognized by the potato resistance protein R3a (published in *Proceedings of the National Academy of Sciences, USA*). This presents the first opportunity to study gene-for-gene recognition and resistance mechanisms in the late blight pathosystem. Studies of allelic diversity in *Avr3a* are stimulating the development of novel disease resistance strategies.

***Phytophthora infestans* population studies** A set of over 1000 *P. infestans* isolates from the UK, and other European states were screened using SCRI's SSR markers to examine the population structure. Together with EU collaborators we developed a data entry tool and database of over 10,000 isolates of *P. infestans* to collate EU-wide data on *P. infestans* populations. A training course on characterising *P. infestans* populations was held at SCRI. In addition, real-time multiplex PCR tests for *Phytophthora* species affecting forests were developed and the protocols are being tested by bodies responsible for UK statutory testing.

Demonstration that multiple independent horizontal gene transfer events from several different sources have driven the evolution of plant parasitism by nematodes Plant parasitism has arisen independently at least three times within the nematodes. Our work has shown that on each occasion important pathogenicity genes, most often plant cell wall degrading enzymes, have been acquired by horizontal gene transfer. Independent transfer events from bacteria to nematodes and fungi to nematodes have occurred during their evolution (published in *Biochemical Journal* and *FEBS Letters*)

Genotyping individuals of *Globodera pallida* (see following article by M.S. Phillips *et al.*).

PCN Management model Five hundred copies of the PCN management model developed at SCRI were released by the British Potato Council to growers and agronomists. The management model allows users to understand the principles governing yield loss and nematode population dynamics. By altering potato cultivar characteristics and cultural practices such as rotation, nematicide treatment etc. future trends in both yields and PCN population levels can be explored.

Climate change is expected to increase pest populations SCRI in partnership with SASA, Rothamsted Research and SAC are studying the ecology of one of the most important agricultural insect pests of potato, the peach-potato aphid *Myzus persicae*. Using molecular techniques that we developed to distinguish genotypes in ecological studies, we have established that there is a constant local population which is supplemented from time-to-time by insecticide resistant forms. We have found that the resistant forms appear to be subject to turnover depending on agricultural practice. With the help of local farmers we have elucidated some of the sources and conditions which maintain insecticide resistant forms in Scotland. In future we will study the underlying effects on potato virus epidemiology. The data generated from this work will provide a useful baseline, not only for changes in the ecology of an agricultural pest, but an insect species that is a widespread indicator of different ecosystems.

The Media Kitchen now managed by the Plant Pathology Programme delivers a wide range of sterile microbiological, mycological and plant tissue culture, media and disposable plasticware across the Institute and operates under ISO 9001:2000 accreditation. The 2005 user survey showed that 100% of respondents rated the service they received as 'good' or 'excellent'. The cost-effective service provides quality assured products (35,000 plates, 41,400 Items, 465,000 Eppendorf tubes and 2,156,000 tips supplied in 2005) and the daily delivery and removal of waste microbiological materials to researchers.

Virus-induced gene silencing: mechanisms and applications

C. Lacomme, J. Shaw, I. Hein, M. Barciszewska-Pacak[a], K. Hrubikova, K. Shirasu[b], A. Molnár[c] & J. Burgyán[c]

Origin of siRNAs in response to virus infection in plants: plant virus-derived small interfering RNAs originate predominantly from highly structured single-stranded viral RNAs. RNA silencing is conserved in a broad range of eukaryotes and includes the phenomena of RNA interference in animals and posttranscriptional gene silencing (PTGS) in plants. In plants, PTGS acts as an antiviral system; a successful virus infection requires suppression or evasion of the induced silencing response. Small interfering RNAs (siRNAs) accumulate in plants infected with positive-strand RNA viruses and provide specificity to this RNA-mediated defence.

It has long been assumed that siRNAs are derived from double-stranded RNA intermediates occurring during the replication cycle of positive strand RNA viruses. This assumption is viewed with some scepticism by researchers involved in virus replication since it is not known if most positive-strand RNA viruses replicate through a completely double stranded RNA, partly double-stranded or predominantly single stranded replicative-intermediate. Moreover, the accessibility by Dicer of double-stranded RNA structure of a replicative-intermediate *in vivo* is questionable. In collaboration with Joszef Burgyán's team we published evidence that siRNAs are unevenly distributed across the viral genome, are mainly derived from the positive-strand, and are imperfect duplexes as would be expected if the siRNAs derived from highly base-paired RNA structures[1].

Several lines of evidence support this model. We previously demonstrated that inverted-repeats folding as hairpin upon transcription enhance the silencing response of positive-stranded RNA viruses, suggesting that formation of dsRNA is a limiting step in the silencing response[2]. Further analysis of siRNA accumulation in plants infected with viruses expressing inverted-repeats indicated that more siRNAs are accumulating than the corresponding antisense sequence. The polarity of the siRNAs was predominantly for the positive strand. A survey of virus specific siRNAs characterized by a sequence analysis of siRNAs from plants infected with *Cymbidium ringspot tombusvirus* (*CymRSV*) indicates that siRNA sequences originate for a large majority from the positive strand and have a non-random distribution along the length of the viral genome, suggesting that there are hot spots for virus-derived siRNA generation. Finally, an analysis of siRNAs derived from two other non-related positive-strand viruses (*Tobacco mosaic virus* and *Potato virus X*) showed that they both display the same over-representation for the positive strand as for *CymRSV* siRNAs. Taken together, these results suggest that virus-derived siRNAs originate predominantly by direct Dicer cleavage of imperfect duplexes in the most folded regions of the positive strand of the viral RNA. By this mean, the siRNA-based antiviral surveillance system would target preferentially the replicative intermediate negative strand for degradation, making this mechanism more effective as such intermediate is much less abundant for replication (See Fig. 1).

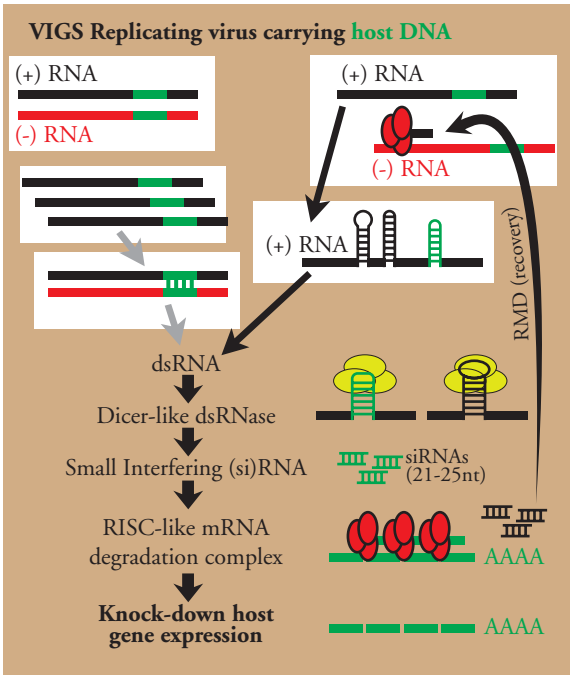


Figure 1 Virus-derived siRNAs originate predominantly from the positive strand as opposed from pairing of negative and positive viral RNA during replication. This in turn makes the surveyance RNA-mediated defence (RMD) mechanism against positive-strand viruses more efficient by targeting the negative strand replicative intermediate in a RISC complex guided by the siRNA, leading ultimately to a recovery phenotype.

VIGS-based functional characterization of genes associated with powdery mildew resistance in barley The properties of this RNA-mediated defence mecha-

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[c]Agricultural Biotechnology Center, Plant Biology Institute, Godollo, Hungary.

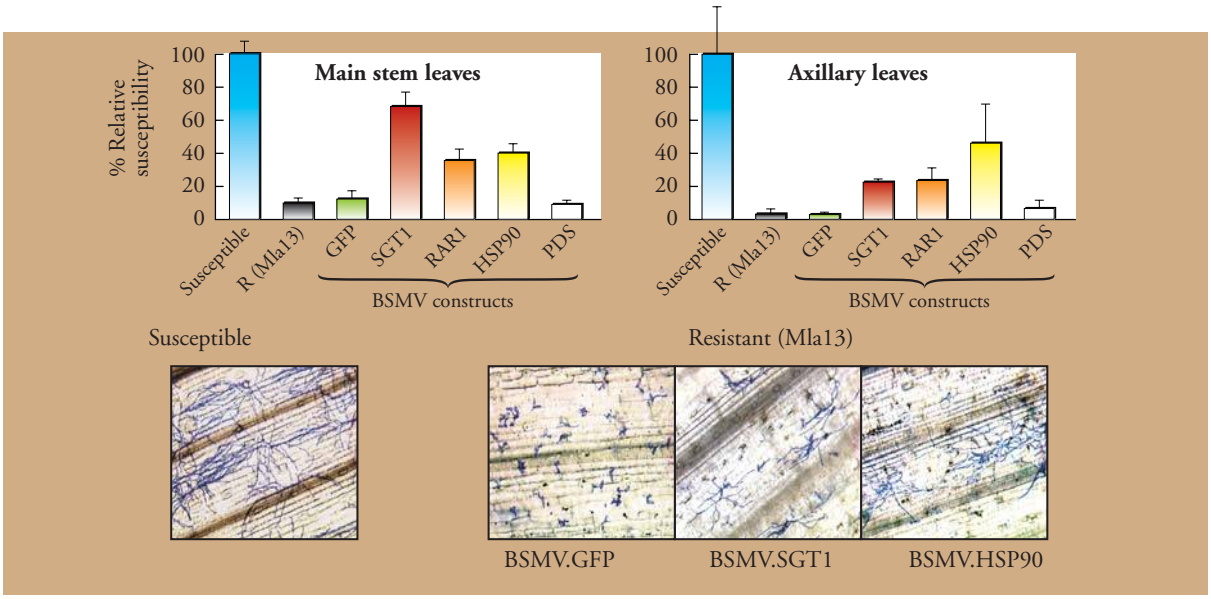

Figure 2 *Rar1*, *Sgt1* and *Hsp90* are required components for *Mla*-mediated resistance in barley to *Blumeria graminis* f.sp. *hordei* (*Bgh*). Percentage of relative susceptibility (to the Susceptible cultivar Golden promise) of BSMV-silenced Sgt1, Rar1 and Hsp90 on resistant cultivar harbouring the *Mla13* resistance gene to *Bgh* (indicative of a resistance-breaking phenotype) in comparison to either BSMV uninfected (R-Mla13) or challenged by a BSMV VIGS construct that does not trigger silencing of genes required for *Bgh* resistance (*GFP* and *PDS*). Observation of typical fungal structures (aniline blue staining) in silenced and control leaves from susceptible (non-infected by BSMV) and resistant barley cultivars infected by BSMV. GFP (no fungal growth) or by BSMV VIGS constructs BSMV.SGT1 and BSMV.HSP90 triggering silencing of respectively Sgt1 and Hsp90.

nism against virus infection offers the possibility to exploit plant viruses as a functional genomic platform based on gene silencing to elucidate plant gene function.

For this purpose, we successfully implemented virus induced gene silencing (VIGS) in barley (*Hordeum vulgare*) for the functional characterisation of genes required for resistance (*Mla*-mediated) towards the biotrophic barley pathogen *Blumeria graminis* f.sp. *hordei* (*Bgh*) (collaboration with K. Shirasu). Mutational analysis and map-based cloning in barley have identified *Rar1* (encoding a small zinc-binding protein with two highly similar domains CHORD-I and –II) and *Sgt1* (encoding a protein that associates with Skp1-Cullin-Fbox type E3 ubiquitin ligase complexes) as being required for *Mla*-resistance to *Bgh*. It has been shown that SGT1 interacts with RAR1 protein and as well with a cytosolic heat shock protein 90 (HSP90). So far the functional proof that *Hsp90* is a required component in disease resistance signalling pathways has been demonstrated only for dicotyledonous plants and is still lacking for *Mla*-mediated resistance in barley. Barley cultivar Clansman (a barley cultivar harbouring the *Mla13* resistance gene allowing *Barley stripe mosaic virus* [BSMV]-VIGS vector replication and systemic movement without causing excessive symptoms), was chosen as the most suitable host for BSMV-VIGS-based functional characterisation of *Rar1*, *Sgt1* and *Hsp90* in the *Mla*-mediated resistance towards powdery mildew. BSMV-induced gene silencing of these candidate genes, which are associated in many but not all race specific pathways, proved to be robust and could be detected at both mRNA and protein levels for up to 21 days post-inoculation. Systemic silencing was observed not only in the newly developed leaves from the main stem but also in axillary shoots. By examining fungal development from an incompatible mildew strain carrying the cognate *AvrMla13*-gene on BSMV-silenced plants for *Rar1*, *Sgt1* and *Hsp90*, a resistance breaking phenotype was observed, while plants infected with BSMV control constructs remained resistant[3].

These findings represent the first evidence in monocots that *Hsp90* is a required component for *Mla13*-mediated race specific resistance and demonstrates that BSMV-induced VIGS is a powerful tool for the rapid characterization of genes involved in pathogen resistance in barley (See Fig. 2).

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Predicting virulence behaviour of *Globodera pallida* populations

M.S. Phillips, M. Elliott, A. Holt, A. Smith, L. Pylypenko, R. Shah, D.J.M. Rodriguez López & V.C. Blok

The two species of potato cyst nematodes, *Globodera rostochiensis* and *G. pallida,* are the most economically important nematode problems of the UK potato industry. They occur in 65% of UK potato land with *G. pallida* present at 92% of these sites[1]. They are difficult to manage because of the persistence of viable cysts in the soil for many years and the lack of resistance in cultivars that are commercially accepted. The increasing pressure to reduce the use of chemicals for their control heightens the need to deploy resistant cultivars effectively. Furthermore, cysts which are spread through movement of farm machinery or non-certified seed tubers establish new infestations which may go undetected for many years until population levels build up and there is evidence of damage to the crop. Effective strategies to control these nematodes and prevent spread are vital to the potato industry.

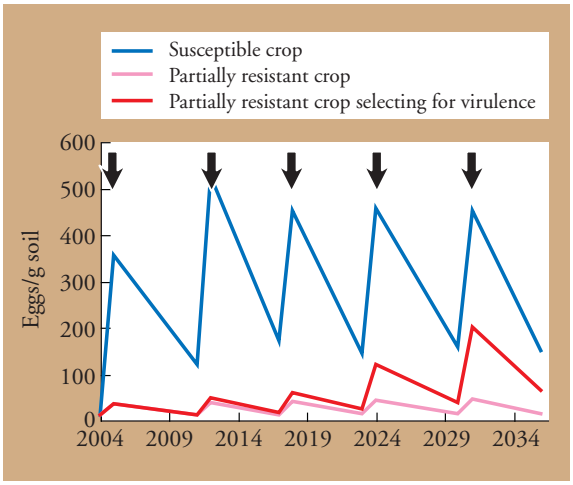

Figure 1 Population trends of potato cyst nematode reproduction if potatoes are grown every six years.

In order to inform advisors and growers, SCRI, with the support of the British Potato Council and a Defra Sustainable Arable LINK project, have produced a computer model which can be used as an educational tool to show how nematode population numbers vary with different control measures such as resistance, rotation length and nematicides. The program can be used to explore different control strategies and shows both the likely changes in nematode population levels and the amount of yield loss that a grower might experience. With the model, possible outcomes of growing cultivars with partial resistance to *G. pallida* can be demonstrated. Because a proportion of *G. pallida* individuals are virulent and able to reproduce on cultivars with partial resistance, the model indicates that growing partially resistant cultivars could limit *G. pallida* population levels but not eliminate them unless a nematicidal treatment or long rotation was also used. There is also the possibility that the nematode populations could be selected for an increasing number of virulent individuals that would render the partially resistant cultivars less and less effective as is shown in Fig. 1. To increase the scope of the model to take account of these potential changes, a population genetics approach is being taken. Molecular features identified that are indicative of the virulence status within a population will enable the monitoring and prediction of population behaviour. This information will increase the utility of the model.

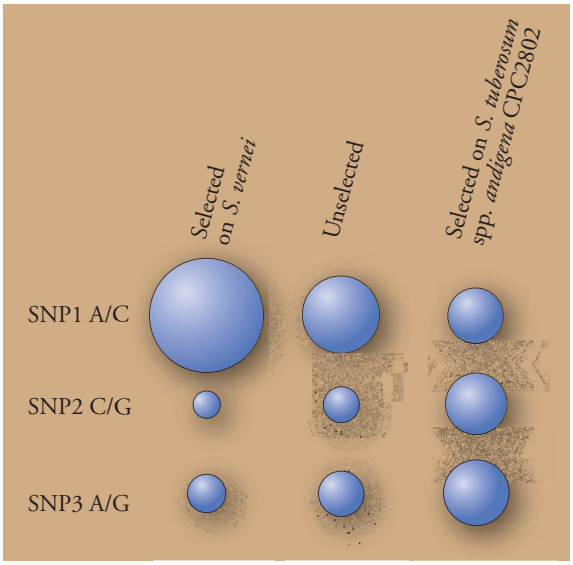

Figure 2 Proportions of A/C, C/G and A/G found in SNP1, 2, and 3 respectively with three PCN populations, unselected, selected on *S. vernei* or selected on *S. tuberosum* ssp. *andigena* CPC2802.

We have been investigating a number of genes that may be implicated in the nematode pathogenicity to see if there is evidence of selection in the sequences (single nucleotide polymorphisms - SNPs) after growth of the populations on resistant cultivars. Sequencing of the chorismate mutase gene revealed that there were a number of changes which affect the amino acid composition of the translation product that could in turn affect the plant response to the translation product. The proportions of variants of three SNPs in different populations have been quantified by pyrosequencing. Compared to the unselected population, the proportion of SNP1 (A) has increased in the population selected on a cultivar with resistance derived from *Solanum vernei* (Fig. 2). In the population selected on a potato with resistance derived from *S. tuberosum* ssp. *andigena* CPC2802, there is a reduction of SNP1 (A) but an increase in SNP2 (C) and SNP3 (A). By looking at a wide range of populations with different proportions of virulent individuals we hope to be able to discover if there are consistent associations between the molecular variation and virulence differences. Such an association would support the idea that the gene was implicated in the nematode/plant interaction as well as being a relatively fast way of monitoring virulence levels within *G. pallida* populations.

Acknowledgements

In the course of this work visiting workers to SCRI have received training and made contributions to its progress; Dr Liliya Pylypenko was a NATO Royal Society Fellow from the Institute of Plant Protection, Ukrainian Academy of Agricultural Sciences, Rujuta Shah and Juan Rodriguez López from India and Spain respectively were M.Sc. students.

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Gastrointestinal stability of raspberry anthocyanins

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Aphid reproduction is modulated by phloem ascorbic acid – novel targets for pest control?

S.D.A. Pont *et al.*

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Quality, Health & Nutrition

D. Stewart

The Programme's activities over the last year have been focussed, multidisciplinary efforts and have addressed combinations of quality and health and/or nutrition. Through collaborations both internally and externally, with academia and industry, SCRI and the Quality, Health & Nutrition Programme are making significant in-roads into establishing the basis and diversity of quality and nutritional parameters in plant-based foods and the beneficial effects that they may have on health.

Research into the basis of the beneficial health effects of plant-based food has focussed predominantly on soft fruit. Intensive *in vitro* studies were undertaken to establish the changes in fruit phytochemicals accompanying digestion and passage through the gastrointestinal tract (GIT). The majority of *Rubus*-derived polyphenols, predominantly anthocyanins and ellagitannins, survived acidic (stomach) digestion but progression through to the upper GIT, where the pH shifts to more alkaline conditions, was accompanied by a dramatic reduction in recoveries. This alkaline-driven degradation produced many smaller, putatively pharmacologically active compounds which would be readily taken up into the blood stream and exert their activities at sites remote from the digestive tract. Interestingly co-incubation and digestion of the fruit (and juice) with other foodstuffs (reflecting normal meal or snack consumption) comprised mainly of polysaccharide (bread) or protein (meat) showed that there was minimal effect on *in vitro* uptake into the serum. This suggests that polyphenols transiently bind to food matrices during digestion, which protects the more labile components, such as anthocyanins, from degradation, and increases their potential serum uptake.

There was also a range of digestive labilities in the *Rubus*-derived phytochemicals with cyanidin-3-*O*-glucoside greatly reduced whilst others, such as pelargonidin-3-*O*-glucoside, were apparently increased in abundance by default. This may have a significant effect on future breeding targets with the digestive stability of specific components a factor to be aware of when assessing potential targets for enhancement.

Studies into fruit health benefits were further extended into *in vivo* studies. In collaboration with the University of Kuopio (Finland) and the Petrov Research Institute of Oncology (Russia) juices from control (yellow, anthocyanin-depleted) and anthocyanin-rich (red) *Rubus* (cloudberry) fruit were fed to young and aged fruit

flies (*Drosophila melanogaster*). Fruit flies are a well accepted and validated model for ageing studies and oxidative-stress related physiological and biochemical phenomena. The studies showed that there was both an age and sex effect evident following the fruit juice consumption. In young female flies there were significant effects of both juices on primary and secondary, more long-term, lipid peroxidation, whereas in young male flies significant reductions in primary peroxidation products occurred with yellow juice and in secondary products with red juice. With the red juice (similar in composition to raspberry), a significant decrease in secondary lipid peroxidation was found in both young and old males, but not older females. The data adds weight to the increasing body of evidence supporting the need to increase the amount of anthocyanin-rich fruits in the diet and, given both the age and sex-related differences, should lead to insights into tailored diets for optimal health and longevity.

Novel polyphenol compounds were isolated and identified in blackcurrant fruit. Their structures are consistent with anthocyanin rutinosides covalently linked to epigallocatechin or gallocatechin. There was also evidence for the presence of a range of other flavanol-anthocyanin condensation products. Overall the contents of these compounds in fruit were roughly correlated to the content of the parent anthocyanins. The conjugates were present in polyphenol-enriched concentrates obtained from both commercially produced concentrates and in fresh extracts of blackcurrants, suggesting that they were not artefacts formed during concentration or purification. Given the reported bioactivity of both the parent anthocyanins and (epi)gallocatechins it is likely that these compounds will exhibit beneficial biological activities and this is currently being tested.

Vitamin C (Vit C) continues to be a focus for research. It is an essential human nutrient that must be obtained in the diet, with the vast majority being obtained from plant foods. A Vit C-deficient diet results in the onset of scurvy, which can have lethal consequences. However, Vit C has also been implicated in the prevention of chronic diseases such as heart disease, stroke, cancer, and several neurodegenerative diseases and as a consequence the dietary allowances for Vit C have been recently increased in several countries. The biosynthesis, regulation and enhancement of Vit C levels in blackcurrant, already a good source, forms one of the programme's research foci.

Studies into the timing and mechanism of Vit C accumulated in blackcurrant fruits have shown that, regardless of the ultimate absolute level, Vit C accumulation was associated with the early phases of fruit development up until fruit started turning red. Following this the levels remained fairly constant. Although up to four Vit C biosynthetic pathways have been proposed in plants, mechanistic studies have shown that only one predominates in blackcurrant fruit. Furthermore, contrary to our previous findings in potato, transport of Vit C from leaves to fruit in blackcurrant makes a negligible contribution to fruit accumulation. Biochemical analysis of high and low Vit C genotypes has demonstrated a clear correlation between biosynthetic capacity during Vit C accumulation and fruit vitamin

content at harvest. The characterisation and mapping of the key genes in the major pathway should help to accelerate the early selection of high Vit C lines in the blackcurrant breeding programme.

Carotenoid and isoprenoid metabolism has long proved to be an attractive target for manipulation since the isoprenoid biosynthetic pathways provide a wide range of metabolites that are essential both for plant development and storage organ-derived food quality. The activities attributed to isoprenoids are multiple and wide ranging. For example, *in planta* they are essential for photosynthesis, membrane stability, phytohormone biosynthesis, plant defence etc. Plant-based foods also contain isoprenoids and specific classes of these, such as carotenoids. The latter have been associated with health benefits, with Vitamin A precursors essential to retard age-related macular degeneration and Xerophthalmia, a major cause of blindness in children in Africa and Latin America. The isoprenoids also exhibit non-health activities and have often been implicated as important determinants of flavour in plant-based foods.

Previous perturbations of the isoprenoid metabolism in potato focussed on expressing the *Erwinia uredovora*-derived *crtB* gene encoding phytoene synthase. This work has continued leading to an elevation of total carotenoids in both *S. tuberosum* and the diploid *S. phureja* of 6- and 4-fold, respectively. In addition transformation with *crtB* was accompanied by radical changes in the balance of the carotenoids with the appearance of β-carotene and a 19-fold enhancement of lutein.

Modifications to the *S. tuberosum* and *S. phureja* carotenoid profiles were also evident following transformation with the algal gene *bkt1*, a β-carotene ketolase (or oxygenase) that catalyses the formation of a carbonyl group at carbon position 4 of each ring of β-carotene. The transformed tubers had elevated levels of the ketocarotenoids ketolutein and astaxanthin. The latter is reported to exhibit anticancer effects and enhance immune function in humans.

All isoprenoids require isopentenyl diphosphate (IPP) for their biosynthesis and so some effort was put into manipulating IPP biosynthesis in potato. A key enzyme in the initial stages of the plastidic pathway of isoprenoid biosynthesis is 1-deoxy-D-xylulose 5-phosphate synthase (*dxs*), the product of which is subsequently transformed into IPP. Transformations of potato with a bacterial *dxs* gene saw the total tuber carotenoid content increase approximately 2-fold, with most of the increase accounted for by a 6-7-fold increase in phytoene. Interestingly, *dxs* expression was also correlated with tuber elongation and an early tuber sprouting phenotype. This is being explored further.

Metabolic profiling continues to underpin much of the QHN science. As part of complementary studies in the Genetics Programme, it is being applied to the Commonwealth Potato Collection to assess phytochemical diversity with the aim of identifying possible new traits for introgression into the breeding programme. This approach has been further refined and, in collaboration with the Genetics Programme and the Federal Centre for Breeding Research on Cultivated Plants Germany, applied to segregating crosses of raspberry and strawberry, respectively. The development and application of Direct Infusion Mass Spectrometry to both projects has allowed rapid, but data-rich, analyses to be undertaken on these large populations and is yielding insights into the interplay and inheritance of polyphenols, Vit C and other nutritionally relevant phytochemicals. This approach is becoming attractive as a rapid high throughput screen for phytochemical population analyses.

Diversification into the non-food crops arena has been assisted by prestigious Scottish Enterprise Proof of Concept (PoC) and subsequent PoC-Plus funding to develop smart screens for wood properties. Current methods of determining and predicting wood properties and composition are both expensive and laborious. The aim of this project was to establish the concept that infrared scanning technologies could be used to predict wood properties and composition. The end use of this technology was multifaceted and included the enhancement of Scottish Sitka timber via earlier screening of the germplasm for density etc. and the ability to identify and quantify wood adulteration, contamination and biodegradation (rot). Using a clonal population of Sitka Spruce, calibrations were constructed between parameters of wood measured in the laboratory and the associated infrared spectra and these were then used to predict the values of these parameters in previously unanalysed samples. The infrared scanning technology was successful in all of the approaches and allowed a reduction in the multifactorial analysis time by at least 100-fold. In addition, the technology was able to successfully detect very low levels of biodegradation and inorganic contamination in wood. As a result of this the use of infrared technologies for predicting and quantifying selected wood properties has been the subject of a patent application and is currently the subject of development to commercialise this approach.

Gastrointestinal stability of raspberry anthocyanins

G.J. McDougall, A. Blake, P. Dobson, P. Smith & D. Stewart

Anthocyanins are the polyphenol pigments responsible for the red to blue colours of plant fruits, flowers and leaves. Berry fruits are rich sources of anthocyanins providing 100-300 mg in a portion. Anthocyanins are effective antioxidants and their intake has been reported to enhance cardiovascular performance, protect against carcinogens, suppress inflammatory responses and protect against ageing-related decline in the central nervous system.

To achieve these body-wide effects, anthocyanins must be bioavailable i.e. available from digested foods, effectively absorbed from the gut into the blood and delivered to the appropriate locations throughout the body. The bioavailability of anthocyanins is open to question. Eating anthocyanin-rich fruits, extracts or pure anthocyanins has beneficial effects in preventing or suppressing disease states *in vivo*. Oral administration of anthocyanins confirmed increased blood antioxidant status but this was accompanied by very low uptake of anthocyanins into the blood (<<1% of dose). The apparent low bioavailability of anthocyanins casts doubt on their ability to exert their proposed beneficial effects.

Assessment of anthocyanin bioavailability requires complex and expensive studies on their absorption, metabolism, and excretion. In this study, we assess the stability of raspberry anthocyanins using a laboratory-based two-stage digestion procedure that mimics the physiochemical conditions encountered in the gastrointestinal tract.

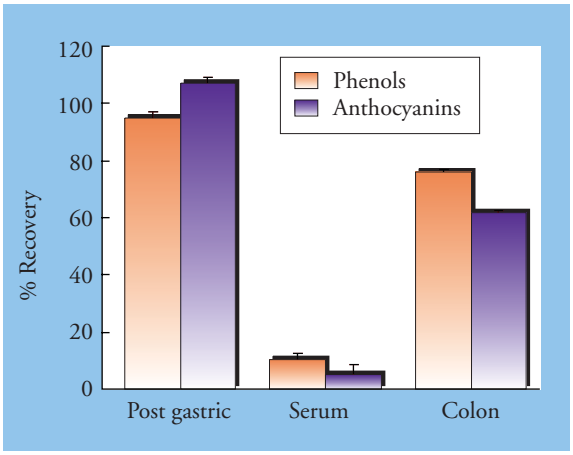

Figure 1 Recovery of phenols and anthocyanins from raspberry after gastrointestinal digestion.

Effectively all of the polyphenols in the raspberry extract survived gastric digestion and partitioned between the serum-available material and the colon-available material after pancreatic digestion. All of the anthocyanins also survived gastric digestion but only ~5% entered the serum available sample and ~65% of total anthocyanins were recovered in the colon available sample (Fig. 1).

Eight anthocyanins, composed of two anthocyanidin core molecules called cyanidin and pelargonidin linked to four different sugar structures (Fig. 2), were detected in the raspberry extract using liquid chromatography mass spectrometry (LC-MS). All eight anthocyanins were completely stable to gastric digestion. All eight anthocyanins also survived the pancreatic digestion but some such as cyanidin-3-*O*-glucoside were greatly reduced and others such as pelargonidin-3-*O*-glucoside were much more stable (Fig. 2). Differences in gastrointestinal stability did not match previous studies on the differential stability of pure anthocyanins. In particular, enhanced stability was not correlated to the anthocyanidin core or the attached sugar structures (Fig. 2). It would appear that in mixtures such as found in natural fruit extracts and juices, certain anthocyanins are sacrificially protected by oxidation of other anthocyanins. The gastrointestinal stability of anthocyanins as measured by this laboratory procedure can be related to the pool size available to transport mechanisms operating in the gut and therefore influences bioavailability. Information on the link between anthocyanin structure and the bioavailability of anthocyanins could be applied to SCRI breeding programmes to produce healthier varieties of soft fruit such as raspberry and blackcurrant.

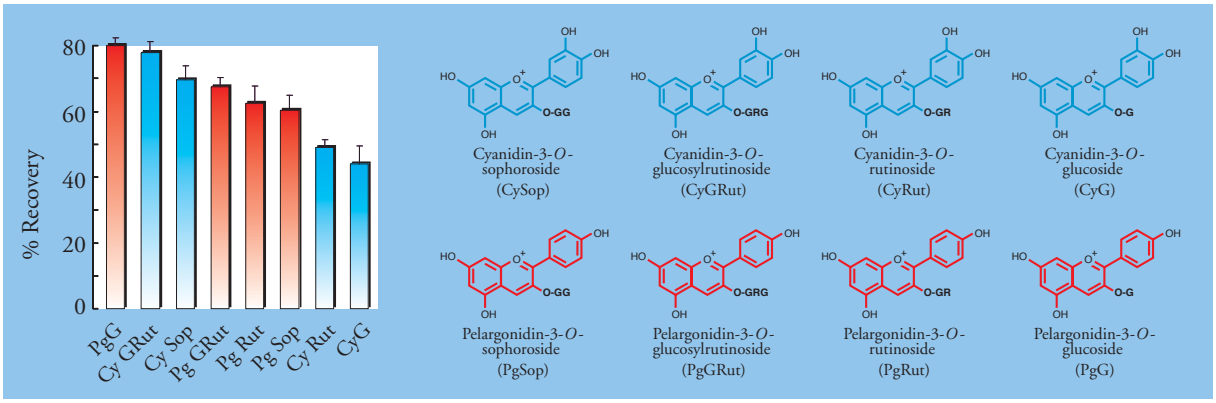

Figure 2 Recovery of individual raspberry anthocyanins after pancreatic digestion. The anthocyanidin core structures are colour coded in blue for cyanidin and in red for pelargonidin.

Aphid reproduction is modulated by phloem ascorbic acid – novel targets for pest control?

S.D.A. Pont, P.G. Walker, S. Lamond, B. Fenton & R.D. Hancock

L-Ascorbic acid (AsA; Vit C) is the most abundant soluble antioxidant found in plants and is also an essential nutrient for humans and a few other animals. Together with flavonoids, polyphenolics and lipophilic compounds such as α-tocopherol (vitamin E), AsA contributes to the overall intake of free radical scavengers in the human diet. Diets rich in fruit and vegetables are associated with decreased risk of certain cancers and cardiovascular diseases and this has been attributed to the high concentrations of antioxidants in such foods. Many of the plant foods consumed by humans are sink organs (e.g. fruits, tubers), non-photosynthetic tissues that receive carbohydrates and other compounds from leaves via the phloem, the transport tissue of the plant. As part of our ongoing investigations into factors contributing towards AsA accumulation in these organs, we undertook a number of studies to investigate the contribution of AsA delivered via the phloem[1,2]. Work undertaken at SCRI and in other laboratories demonstrated that AsA was a major component of the phloem sap and hence transport of AsA from leaves to fruits or tubers was a mechanism by which the compound may accumulate in these organs. An additional implication of our findings was that phloem feeding insects such as aphids would be exposed to a diet rich in AsA. This led us to consider what impact phloem AsA might have on phloem feeding insects.

Figure 1 Aphid cage used in this study. The leaf petiole is placed into the reservoir shown at the foot of the image.

Aphids are major world pests on many food and commodity crops. The peach-potato aphid (*Myzus persicae*) is a pest on many crops worldwide and is of particular relevance to the UK potato industry as it represents the major vector for a number of viral diseases affecting the seed crop. We therefore chose to examine the role of AsA in modulating the reproductive success of *M. persicae* colonies grown on potato leaves. Single potato leaves were transferred to small aphid cages and the leaf petiole passed through the bottom of the cage into a reservoir (Fig. 1). The reservoir contained either water or solutions of L-galactono-1,4-lactone (L-GalL) the immediate precursor of AsA in plants. A single one-day-old nymph was transferred to the potato leaf and allowed to develop for 15 days. At the end of the culture period, the nymph had matured to an adult and

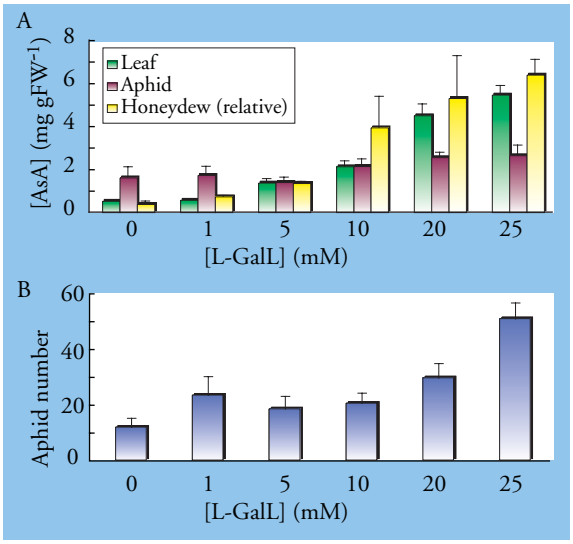

Figure 2 Increasing concentrations of L-galactono-1,4-lactone in leaf reservoir buffer result in increased AsA concentrations in leaves and aphids and in the capacity of aphids to grow and reproduce.
Panel A: The x-axis shows the concentration of L-GalL in the reservoir buffer and the y-axis shows the concentration of AsA found in leaves (mg gFW^{-1}), aphids (mg gFW^{-1}) or aphid honeydew (relative amount). Bars represent mean values ± SE (n=10).
Panel B: The x-axis shows the concentration of L-GalL in the reservoir buffer and the y-axis shows the number of aphids recovered 15 days after inoculation of leaves with a single one-day-old nymph. Bars represent mean values ± SE (n=10).

had started reproducing. The number of aphids present was recorded and the AsA content of leaves, aphids and aphid honeydew (material secreted by the aphid after nutrient absorption) was determined. Addition of L-GalL to the reservoir resulted in a dose-dependent increase in the leaf AsA. Increased leaf AsA concentration resulted in an increased AsA concentration in both aphids and aphid honeydew (Fig. 2A). This demonstrates that there was increased availability of AsA to aphids from the phloem. Furthermore, increasing the AsA concentration in potato leaves had a dramatic effect on the number of aphids recovered at the end of the experiment rising five-fold between the lowest and highest leaf AsA concentrations (Fig. 2B). These data show for the first time that the ability of aphids to grow and reproduce on potato is enhanced when higher concentrations of AsA are present in the phloem.

In insects AsA has been implicated in a number of physiological functions however, despite many years of research, there is still no consensus regarding the capacity of insects to synthesise AsA with contradictory reports regarding insect AsA requirements. Our data suggest that when feeding directly from plants the quantity of AsA present in the phloem may be insufficient to support maximal growth and reproduction in *M. persicae*. However, there was a close correlation between leaf AsA concentration and the amount of AsA secreted in aphid honeydew suggesting that surplus AsA was available to aphids even at the lowest leaf AsA concentrations. An alternative mechanism by which AsA could modulate aphid success is through the removal of reactive oxygen species that may be present in the phloem and act as a deterrent to aphid feeding. These compounds are highly reactive and may damage the aphid causing the insect to stop feeding to allow recovery. Due to its antioxidant properties, increased phloem AsA would reduce the prevalence of free radicals. In turn, this could allow the aphids on AsA rich diets to feed for longer periods and therefore absorb more nutrients over the same time period as the control insects. The net result would be an increase in reproductive potential due to a shorter development period, increased availability of nutrients for reproduction or a combination of the two.

Current work is aimed at further understanding the mechanism by which phloem AsA modulates aphid success. A thorough understanding of the interaction at the biochemical, molecular and physiological levels will provide novel targets for breeding aphid resistant cultivars and for the development of novel pesticides.

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Environment Plant Interactions

B. Marshall

Concerns for the environment we live in and interact with were formally recognised at the World summit meeting in Rio in 1992 resulting in the Convention on Biological Diversity. 150 world leaders agreed a comprehensive strategy for 'sustainable development', two of the three key goals being the 'conservation of biological diversity' and 'the sustainable use of its components'. More than a decade later we are now seeing these goals being addressed on many fronts. The management of agricultural and especially arable land is undergoing major changes in the light of reforms to the Common Agricultural Policy (CAP) for Europe. These reforms are driven both by economic needs of the EU and its members as well as concerns for the environment. Scotland has seen the launch of the 25 year programme, 'Scotland's Biodiversity in Your Hands', which places a responsibility of care for the environment at the forefront of national and local government planning, public bodies and commercial activities that may impact the environment. The CAP Reform has already introduced 'Decoupling' and 'Modulation'. Through decoupling farm businesses no longer receive subsidies for the production of specific food stuffs. Instead the farmer receives a single farm payment. Initially the amount of single farm payment paid to a business reflects the previous levels of subsidies received. However, it is independent of any future crops grown. More significantly, the concept of modulation will determine increasingly the transfer of money towards payments directed at activities that build a more environmentally sustainable future for the industry e.g. by paying farmers to farm in a way which promotes biodiversity.

Two thirds of all land in Scotland, some 2.9 million hectares, is classified as agricultural of which one fifth is arable. Much of the human population in Scotland lives in or is close by this arable land. The opportunities for enhancing this environment for both the benefit of the public and the longer term sustainability of the managed systems are considerable. Arable land is often the most intensively managed. On average in Great Britain, an arable crop receives ten spray applications of pesticides (note two pesticides in a single mixture counts as two applications) during its lifetime. These are predominantly fungicides and herbicides and, to a lesser extent, insecticides, desiccants and seed treatments[1]. While the number of applications has gone up the rates have gone down, so that total amounts of pesticides applied are also declining – reduced inputs used

more efficiently. The conservation and enhancement of biodiversity and the saving of particular species from extinction are seen as key objectives by the public, including many farmers. Biodiversity has become almost a mantra. In drafting advice for policy makers and producers, it is essential that we can take an objective and informed view of how changes in biodiversity, both the quantity and composition, affect the sustainability and resilience of managed systems. Through understanding how biodiversity relates to system function one is in a better position to define how best to measure changes in the environment and manage it better. It is also inescapable that such systems must be socially and economically sustainable.

The central theme of the **Environment Plant Interactions** Programme is 'The efficient use of resources in sustainable and resilient managed systems' with the emphasis on the arable sector and the landscape it resides within. Key resources are water, carbon, nitrogen and phosphorus which are brought together in a common currency of energy. Energy is ubiquitous in the agro-ecosystem e.g. solar radiation is the energy driver of primary production through photosynthesis, as stored energy held in the various chemical compounds produced within the plant; energy is transferred from one organism to another through root exudation, herbivory, predation etc. Energy is also consumed in the production of chemicals, their transport to the farm and in agricultural operations on the farm. Similarly energy is consumed when products are either recycled on the farm e.g. manure, or transported off the farm as products. In order to assess the relative sustainability of alternative managed systems one has to take a holistic view. Sustainability is the ability to hand on to successive generations managed systems that remain environmentally 'healthy' and economically viable. The environment includes above and below ground biodiversity and its functioning. The resilience of a system is the ability to tolerate perturbations such as extremes of weather, pollution events or introduction of a new management practice and still be able to return to its original dynamic state.

The Programme's research activities divide into three main areas: Plant and plant-soil interactions, Functional ecology and Ecosystem upscaling. Each research area stands on its own merit and gives added value by being committed and contributing to a core theme. Within the SEERAD strategy, the Programme makes significant contributions to Sustainable Crop Systems, Soil Quality and Soil Function, providing underpinning science for Protecting Biodiversity and Environmental-Sustainability.

Within **Plant and plant-soil interactions** the plant is seen as the central driver through which the agro-ecosystem is manipulated both through genetic manipulation of the crop plant and the way in which the crop is managed both in space and time. Areas of research include

• Soil structure and strength, which are key to a sustain-

able soil and strongly influenced by the plants and associated microbial communities that grow in it.

- Root development and exploration, which determine the spatial and temporal availability of resources both to the plant and from the plant to the soil microbial community.
- Resource acquisition, partitioning and utilization by plants, which are central to the quantity and quality of resource flows through the system and the food-webs that depend upon them.

Within **Functional ecology** the primary focus is the relation between the diversity of functional traits and key system processes: resource capture by plants and cycling of this energy, carbon and nutrients through the system via the soil and arable food webs. The overall goal is to identify sets of plant traits and their management which optimise the productivity, sustainability and resilience of the system. Two, frequently implicit, assumptions to be tested in this research are that functional diversity is more important than biodiversity *per se* and that the greater the diversity of organisms within a functional group the more resilient that process is. While a system with low diversity will have low functional diversity the converse is not necessarily true. A system comprised of many species does not necessarily mean that that system is necessarily functionally diverse. Equally, one should not ignore the diversity within species. The diversity within species is at least as important as the diversity between species. Plant breeders depend upon the diversity within a species to discover new genes that, for example, confer added disease resistance to or improve nutritional quality of new cultivars. Both above (crop, weeds, herbivores and predators) and below (roots, nematodes, N-cyclers and AM fungi of soil function) ground food webs are being studied using a combination of approaches including:

- Trait-based approaches to quantify the links between diversity and system function.
- Molecular techniques to determine the genetic basis for phenotypic variation within and between species or groups.
- Ecological impact of changes in management practices on functional diversity (above and below ground), temporal stability and productivity.
- Root exudates and root biophysical properties affecting soil-dwelling herbivores and associated feed-back mechanisms.
- Soil resilience: critical factors affecting soil biological and physical resilience.

Ecosystem upscaling is essential to be able to predict at farm- and regional-scales, the impact of a new crop variety or a change in field practice on factors such as carbon sequestration, food web activity, biodiversity, and genetic containment. In the reverse direction, predictive capability is needed to assess the effect of 'global' changes (climate, deposition, new pesticides) on the requirement for and efficacy of new crop varieties and practices. Indeed, most questions of policy are asked at these large scales (climate change, biodiversity, invasives). Initial studies will proceed both through analysis of existing extensive databases in Great Britain and the European Union and new measurements of targeted processes (energy/carbon dissipation), communities (arable plant biodiversity) and target organisms (e.g. wild and feral crucifers). The following generic topics extend the trait-based modelling of resource flows at plant and patch scales to the ecosystem:

- Assessing the sensitivity of main biophysical factors at field- and landscape-scale to new biotechnology.
- Predicting best field practice and crop cultivars to stabilise food webs over the rotation.
- Spatial-temporal characterisation of the SCRI's 'regional study areas' in Angus.
- Developing a generic modelling framework for determining how a process upscales, e.g. how a change in crop variety affects the wider environment.

The knowledge and expertise generated by the programme reaches out to many sectors in Society, as well as the scientific and commercial sectors, where it plays a strong role in influencing policy e.g. the Defra Farm Scale Evaluation trials and gene flow, and public. Most recently we have been working on a suite of new, exciting resources to inform schoolchildren and the general public about the importance of the environment, agriculture and science. The result is the Living Field CD, a multi-media project based on the Scottish Executive's 5 - 14 National Guidelines for Environmental Studies: Science. It contains more than 300 pages of high quality images, sound, games and activity sheets to reinforce the curriculum. The CD has been distributed to all Scottish Primary and Secondary schools and it has been received enthusiastically by teachers, pupils, parents and education advisers alike.

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Management impacts on arable diversity and function

R.E. Wheatley, C. Hawes, T.J. Daniell & A.N.E. Birch

Loss of biodiversity has the potential to disrupt a range of agro-ecosystem functions such as nutrient cycling, population stability, system productivity and resilience. Examples include biocontrol of pests and diseases by natural enemies, pollination of crops and wild plant species and long term soil productivity. Such functions are essential for sustainable agriculture, and economists place an extremely high value on these ecological services globally; pollination of crops has an estimated worth of $117 billion, biocontrol around $400 billion and soil nutrient cycling is valued at over $3 trillion, per year[1]. Studies of the relationships between biodiversity and system functioning have indicated that as diversity increases so does resource use efficiency and system resilience to stress – both abiotic, e.g. shortages of water, nutrients, and energy, and biotic, e.g. pest epidemics and invasion by alien species. We have adopted a functional trait-based approach to quantify the link between diversity and function in arable systems, to determine the impact of management on this diversity.

In order to quantify the relation between diversity and function in arable systems we are developing a novel approach where organisms are characterised by functional traits that are important in energy and nutrient cycling. This approach is applied to whole field arable systems, from soil organisms and processes to whole plants and communities, and to invertebrate primary and secondary consumers. This is illustrated by two examples of recent research in the Environment Plant Interactions Programme.

Functional diversity in above-ground arable food webs Resilience and productivity in arable systems depends to a large extent on the characteristics of the system components with respect to a given process or function, and are thought to increase with functional diversity. We are quantifying the relation between functional diversity and system properties (energy flow and productivity), by classifying individual organisms according to functional traits that relate to resource acquisition and transfer. For arable weeds, functional

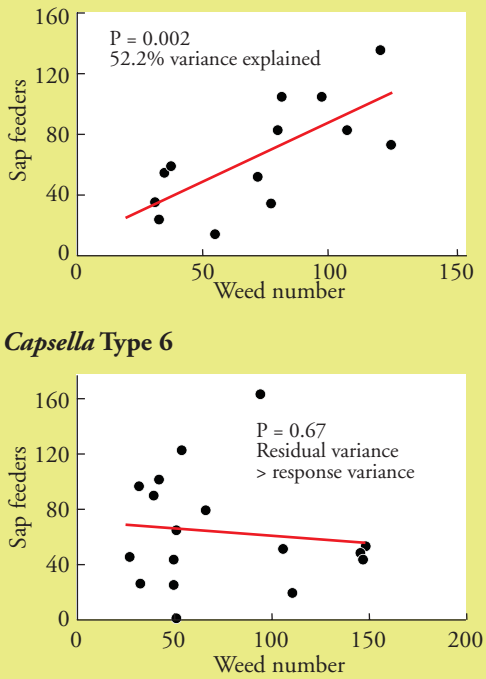

Figure 1 Within and between species variation in functional traits of plants and the impact on higher trophic groups was assessed at the patch scale. The positive relation between plant biomass and herbivore number in Ecotype 1 was not found for Ecotype 6 suggesting that there are differences between *Capsella* ecotypes in the quality of resource presented to insect herbivores.

traits include architecture (height and spread), determinacy, time from germination to flowering, annuality, development rate and nutritional characteristics that affect insect herbivores (host quality). At the field scale, we have shown that the abundance and functional diversity of arable weeds is affected by management practices and the type of crops sown. Changes in the amounts and quality of this weed resource have a significant impact on the abundance of the insect community. Work is in progress to explore the mechanisms behind this relation between plant and insect functional diversity and to determine the impact of functional diversity across all trophic levels on system properties (Fig. 1).

Spatial and temporal variation in soil microbial functioning Potential Nitrification Rates (PNR) estimated over the growing season of spring barley showed large spatial and temporal variability. Although there were large dynamic changes in PNR between sampling occasions certain areas within the field were always relatively high or low. Whole soil nucleic acid extracts were taken at such points, and PCR cloning in conjunction with a high-throughput sequencing approach targeting a fragment of the ammonium mono-oxidase A *(Amo-A)* subunit gene was performed. A neighbor-joining tree of all clones showing phylogenetic relationships between groups (Fig. 2) revealed that all detectable nitrifying bacteria at this site were of the *Nitrosospira* genus, not the classic nitrifying, closely related *Nitrosomonas* genus, and that the distribution of nitrifier types varied both with space and time.

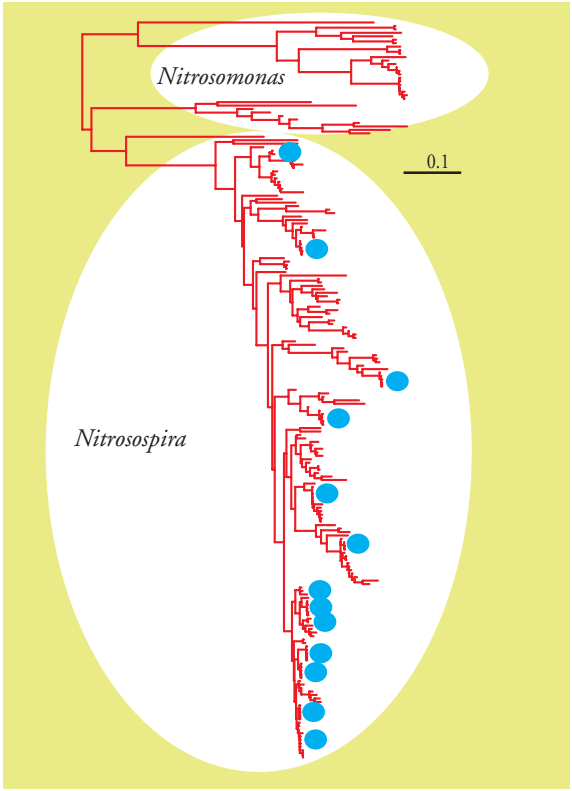

Figure 2 A neighbor-joining tree of all clones showing phylogenetic relationships between the nitrifiers, over time and space, in the field.

Experiments are in progress to investigate the drivers behind the observed diversity differences in both these examples. This will enable us to define the level of functional diversity necessary to maintain resilient, sustainable and productive agro-ecosystems.

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The resilience of soil to biological and physical stresses

P.D. Hallett, H.L. Kuan, B.S. Griffiths, A.S. Gregory[a], C.W. Watts[a] & A. Whitmore[a]

The key to soil sustainability is an ability to resist and recover from the stresses imposed by man and nature. Measures of the stability of soil have therefore received considerable research interest, but measures of resilience are only just emerging. Little is known consequently about the soil properties that contribute to resilience or the influence of antecedent soil conditions on physical and biological responses to stress. A joint project between SCRI and Rothamsted Research has developed novel methods for assessing the biological and physical resilience of soils, which have allowed us to start to unravel the complex processes involved in the recovery of soils from stress.

There have been several stages to this research: (1) development of simple laboratory based resilience assays, (2) application to a wide range of Scottish soils, (3) controlled field experiments where the soil has been exposed to different physical stresses and (4) laboratory studies to investigate the role of different soil properties. Our biological stability and resilience indices examine shifts in the ability of soil organisms to decompose carbon. They are measured from the time-dependent effects of either (i) a transient stress (heating to 40 ºC for 18 hr) or (ii) a persistent stress (amendment with copper sulphate ($CuSO_4$)), on carbon decomposition of added plant residues. Our physical stability and resilience measures are: (i) compression and expansion indices of the soils to assess potential compaction impacts; and (ii) resistance of the pore structure to overburden stresses under prolonged wetting and structural regeneration through cycles of wetting and drying. By measuring both biological and physical resilience, we are able to investigate how soil organisms influence and stabilise the physical habitat in which they live.

A study of Scottish soils examined 26 different locations from the Central Belt to Shetland (Fig. 1). A wide range of biological and physical resilience responses were observed. Decomposition of plant residues following heat or copper stress after one month of recovery ranged from 23% to >100% that of the unperturbed soil. The air-filled pore space after the overburden stress ranged from 70% to >100% of the unperturbed soil. We were hoping that this survey of many soils would help us elucidate the major properties of soil that confer stability and resilience. The only trend observed was from

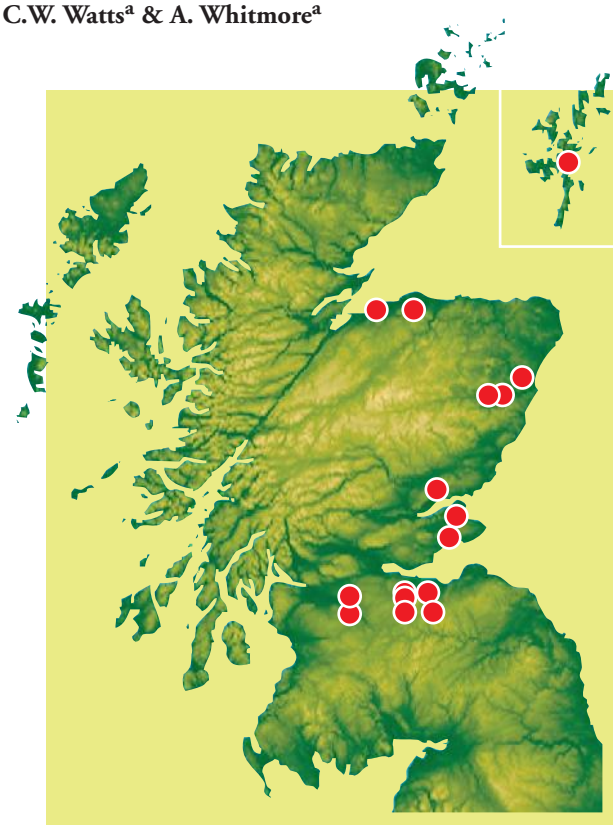

Figure 1 Soil was sampled from 26 sites across Scotland on soils ranging from wind-blown sands (Aeolian) to upland peats.

the influence of carbon, which was related to the resilience to copper stress and both physical measures. The stability and resilience of these soils to compaction are illustrated in Fig. 2. Greater carbon has a negative impact on stability to compression and although carbon also increases resilience, very little recovery occurs following this stress. The persistence of soil compaction is often observed in arable soils.

This survey of Scottish soils included serpentine, aeolian sand, peat and arable mineral soils, so the inherent properties varied markedly. A more controlled field experiment, discussed in the preceding article by Wheatley R.E. *et al.*, investigated the impact of physical disturbance of one soil type through different forms of soil cultivation on biological resilience. Soils under minimum and zero tillage were less stable to the transient heat stress compared to ploughed, deep ploughed and ploughed-compacted soils, but recovered rapidly

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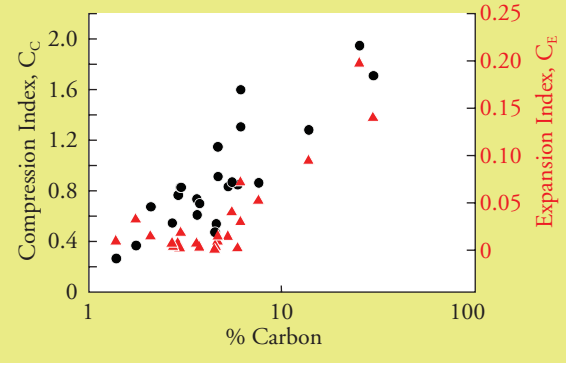

Figure 2 Soil compresses and recovers more as the carbon content increases. The compression and expansion indices, C_C and C_E respectively, are related to the amount of pore space lost for a given level of compaction stress.

to much higher levels (Fig. 3). Less clear trends were found for the persistent copper stress, although the most physically disturbed deep ploughed and ploughed-compacted soils continued to degrade with time, whereas the other soils stayed static or showed signs of recovery. This study suggests benefits to biological resilience by reducing physical disturbance through cultivation. We are beginning to investigate if changes to the microbial community or soil physical structure are driving these changes. An on-going study of the stability and resilience of Rothamsted Research's long-term experimental plots, some dating back to 1843, will give greater evidence of the role of soil management.

By manipulating soil properties in the laboratory, we have isolated some of the dominant properties of soil that control its stability and resilience to stress. An experiment where the microbial communities were 'swapped' between two physically different soils showed the large impact of the pore space and particle surface area on the microbial community that develops and

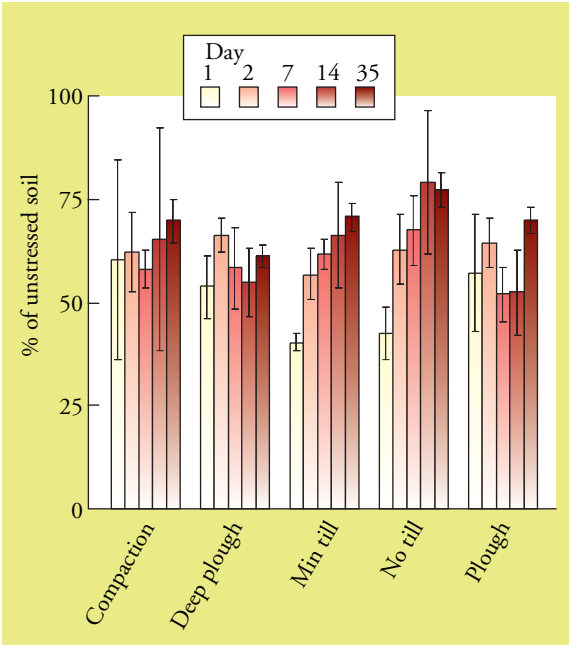

Figure 3 Reducing physical disturbance by using minimum or zero tillage resulted in soil less stable but far more resilient to heat stress. The days since the stress was applied are indicated by the different coloured bars.

its subsequent stability and resilience to stresses. The physical condition of the soil when a stress is applied is also extremely important. Water potential and the habitable pore space for microbes have a major impact.

Our stability and resilience assays have provided useful indicators of soil quality. Massive differences in soil resilience were found across Scotland, which could not have been predicted using data available in existing soil surveys. Current changes in soil cultivation practices towards reduced tillage may help improve the resilience of our arable soils. It does appear that improving the physical stability and resilience of soil has positive implications to biological processes.

The hidden half: marine primary productivity

J.A. Raven *et al.*

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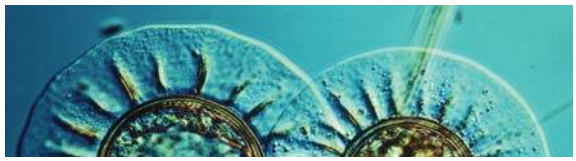

Plant Research Unit, University of Dundee

C. Halpin & G.G. Simpson

Since its move to SCRI two years ago, the Plant Research Unit of the University of Dundee continues to grow with the first joint appointment, Dr. Gordon Simpson, made in late 2004. The Unit now constitutes 5 Principal Investigators with a combined research staff of 20 people. The Unit is part of the Division of Environmental and Applied Biology within the University's School of Life Sciences. The School received the highest possible, 5 rating in the most recent research assessment exercise and, in 2005, was once again voted the best place to work in Europe by readers of The Scientist magazine. The research interests of the Division of Environmental and Applied Biology include basic studies in microbial, plant and animal ecophysiology and molecular biology complemented by more solution-focussed projects in environmental biotechnology. The work of the Plant Research Unit, like that of the rest of the Division, impacts on issues of major public concern such as biodiversity, the impact of climate change on plant productivity, and the benefits and risks of plant biotechnology.*

The Plant Research Unit comprises five research groups with major interests in:

- Transposons, genome evolution and biodiversity in plants (Dr Andy Flavell)
- Manipulation of plant metabolism using reverse genetics (Dr Claire Halpin)
- Plant ecophysiology and adaptation to environmental stress (Prof. Lyn Jones)
- How photosynthetic organisms acquire carbon (Prof. John A. Raven FRS FRSE)
- Regulated gene expression controlling floral development (Dr Gordon Simpson)

Transposons One major thrust of the unit's research is to understand how plants adapt to diverse environmental stresses. The underlying genetic variation within a species – its biodiversity – that enables such adaptation, is the focus of Dr Andy Flavell's research. This biodiversity, encoded by the different DNA sequences in all the individuals of that species, has built up over millions of years via naturally arising mutation and natural selection. Mobile genetic elements, known as transposons, have emerged as dominant factors that underly this biodiversity in plants and many other eukaryotes. Dr Flavell's group is interested both in the basic biology of these genetic

elements and in exploiting them as molecular markers for genetic and genomic studies in plants, since one of the big problems facing biodiversity research is the measurement of genetic variation across thousands or millions of organisms. An important offshoot of the marker studies has been the extension of the transposon-based marker technologies to accommodate single nucleotide polymorphism (SNP)-based molecular markers, greatly expanding the scope of the methods. This aspect of Dr Flavell's work has recently resulted in the award of a large EU Framework 6 grant (BIOEXPLOIT; joint value to SCRI/UoD £1.25 million) to collaborate with researchers at SCRI to exploit high throughput SNP marker technology for the improvement of fungal resistance in wheat and potato. Other collaborative work with SCRI to create the GERMINATE database for storing, manipulating and displaying data related to plant biodiversity has also been extremely successful and the database has already been adopted by several EU projects (GENE-MINE, TEGERM, BIOEXPLOIT). Work to further develop the database will continue under BIOEXPLOIT.

Plant ecophysiology Prof. Lyn Jones takes a more ecophysiological approach to understanding specific plant stress responses in a broad spectrum of research that extends from genetic and biochemical studies of salt and heat tolerance through to environmental and climatic modelling and remote sensing. A particular focus of the work is to determine the genetic and ecophysiological basis underlying differences in the growth and distribution of wild and crop plants and for predicting the consequences of global climate change. A key theme is to understand the role of plant water relations and of processes such as photosynthesis, stomatal closure, osmoregulation, root growth and changes in hydraulic function in plant adaptation to drought. One aim of this work is to identify the genetic basis of tolerance of drought and salinity as an aid to crop improvement programmes. In the past year, Prof. Jones' group, in collaboration with a visitor from Russia, Dr Vysotskaya, and colleagues at SCRI, has made significant advances in understanding the genetic basis of salinity tolerance in barley. This included identification of genotypic variation in gene expression responses, which is now feeding into a collaborative mapping study of the most interesting genes. Significant advances were also made in understanding heat tolerance of the photosynthetic system by identifying clear differences in physiological response between tolerant and sensitive species. This work involved another international visitor, Dr Stasyk (Ukraine). Prof. Jones' group has also continued their development of thermal imaging and image analysis as a tool for studying stomatal behaviour and stress responses. This work has formed the basis for a £1.5 million HORTLINK project that has just been awarded to develop automated irrigation control systems and work also continues on a major Defra contract (£1.4 million total) to develop new irrigation technologies for field crops. These projects aim to improve agricultural and horticultural sustainability in the face of environmental stresses including potential climate change.

Oceanic absorption of carbon As well as potentially influencing climate, the excess carbon dioxide being released into the atmosphere by human activities is

being absorbed by the oceans, making them more acidic. This threatens the survival of many species and ecosystems. Prof. John Raven (FRS FRSE) chaired a Royal Society Working Group on the problem in 2005. Their subsequent report warns that acidification of the world's oceans has already increased to a level that is irreversible in our lifetimes and recommends that a major international effort be launched into this relatively new area of research, and that action needs to be taken now to reduce global emissions of CO_2 from human activities. Prof. Raven expands on aspects of his current research on marine photosynthetic organisms, including work on the effects of increased carbon dioxide on phytoplankton (see following article by Raven, J.A. *et al.*).

Control of floral development Researchers within the Plant Research Unit also focus on fundamental aspects of plant development, principally flowering and lignification. Dr Gordon Simpson's lab studies the mechanisms by which plants control floral development. To do this, he uses the model plant *Arabidopsis* as well as important cereal crops like rice and barley. This year, Dr Simpson's lab has focussed on three research areas. First, they have studied how one particular RNA binding protein, FPA, promotes flowering. Second, they have isolated new early flowering mutants of *Arabidopsis* in order to detail the connections between genes that control flowering time and those that promote floral development. Third they have studied barley mutants that are unable to properly control the number of flowers (and hence the number of grain) they make. This work makes use of the extensive collection of Optic barley mutants at SCRI. Dr Simpson's research has got off to a flying start with the recent award of a BBSRC research grant and a Strategic Studentship in Crop Science (one of only ten awarded over the whole of the UK). In 2005 Dr Simpson was appointed to the BBSRC Small Grain Cereals Steering Committee.

Biosynthesis of lignin Dr Claire Halpin is also using the Optic barley mutants in her work to understand how plants make lignin. Although the sequence of biochemical reactions on the lignin biosynthetic pathway were first outlined over 40 years ago, recent biochemical and molecular studies have revealed many errors and the pathway is currently undergoing revision. The approach taken by Dr Halpin's group to investigate the pathway is to produce transgenic plants where key lignin biosynthetic genes have been manipulated. This has proved to be an extremely powerful tool and has also led to ideas about how to improve plant raw materials for agricultural and industrial processes. A new area of collaborative research with SCRI in 2005 has been to investigate the potential of lignin manipulation in barley for improving its digestibility as an animal feed or as a raw material for biofuel production. Collaborative work with Prof. David Hopkins (Stirling University) has focussed on the potential ecological and environmental impacts of transgenic trees and crops with modified lignin. Dr Halpin's group has also progressed projects to develop enabling technologies for 'clean' plant transgenesis, such as gene targeting, and has recently won a Commercialization Award from Scottish Enterprise Tayside and the University of Dundee to further this work.

The hidden half: marine primary productivity

J.A. Raven, K. Brown & M. Mackay

Half of the photosynthetic primary productivity on Earth occurs in the ocean. 98% of marine primary production is carried out by phytoplankton. These are photosynthetic organisms, almost all less than one mm long, in the upper few tens or hundreds of metres where sufficient light penetrates to allow rates of photosynthesis in excess of the rates of processes that remove the organic matter produced. The remaining 2% of marine primary productivity involves seaweeds and other photosynthetic organisms attached to the small illuminated fraction of the ocean floor. The marine primary producers are very diverse, in terms of the higher taxonomic levels (Phyla, Kingdoms). By contrast, terrestrial photosynthetic organisms are almost all so-called 'higher plants' (Embryophyta) from the Kingdom Plantae. Fig. 1 shows the number of formally described species, and the range of higher taxonomic levels involved, in primary productivity in the ocean, in freshwaters and on land. Fig. 2 shows examples of some of the major eukaryotic groups represented in the marine phytoplankton. This great diversity of higher taxa represented in the marine phytoplankton is a challenge to those of us who seek to understand the co-existence of these organisms with their different evolved approaches to living in what, at first glance from land-based observers, seems to be a rather homogeneous environment. Complete genome sequences are helping such mechanistic investigations, but so far only a handful of cyanobacterial sequences and one diatom sequence have been formally published.

Much of the senior author's work on marine (and freshwater) photosynthetic organisms has centred on the means by which they acquire inorganic carbon in photosynthesis, and the interactions of carbon acquisition processes with the supply of resources such as light and other nutrient elements. This may seem to be an arcane pursuit in view of the high concentration of inorganic carbon (carbon dioxide and the ionic compounds with which it equilibrates in solution) in seawater relative to that of other nutrients, and the stoichiometry in which the various elements are required by the organisms. However, the concentration and diffusivity of carbon dioxide in water are relatively low, and the general absence of limitation of marine primary productivity by inorganic carbon supply involves the operation of a range of 'carbon concentrating mechanisms'. Some of the research in our laboratory and with co-workers in the University of Sheffield addresses the possibility of a mechanism of inorganic carbon acquisition in marine phytoplankton resembling that of C_4 land plants such as maize and sugarcane. Work in our laboratory, and elsewhere, shows that the operation of these carbon concentrating mechanisms is changed by the supply of other resources. A low light supply for growth decreases the engagement of these concentrating mechanisms, while a restricted supply of other nutrient elements usually increases their engagement. Many of these effects can be rationalised in terms of models developed here on resource costs of building, and operating, the photosynthetic apparatus. However, such rationalisation is not the same as showing the significance of these effects in natural selection. Several publications, with collaborators elsewhere, from our laboratory in 2005 present new data on carbon concentrating mechanisms and their interaction with environmental influences

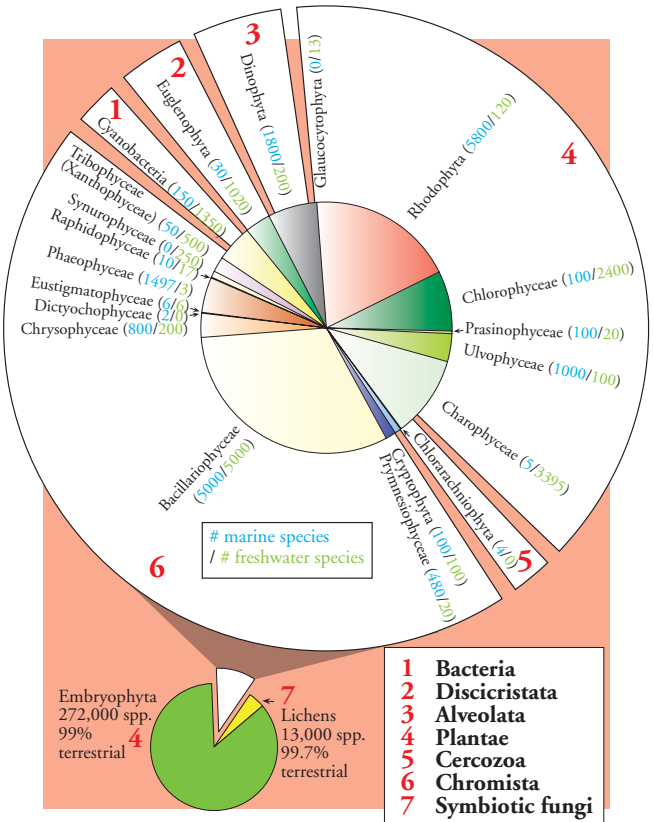

Figure 1 The phylogenetic distribution of terrestrial and aquatic photosynthetic oxygen-evolving organisms. The deep phylogenetic diversity in the aquatic organisms contrasts with the more restricted diversity of those on land, which are almost all embryophytic plants.[1]

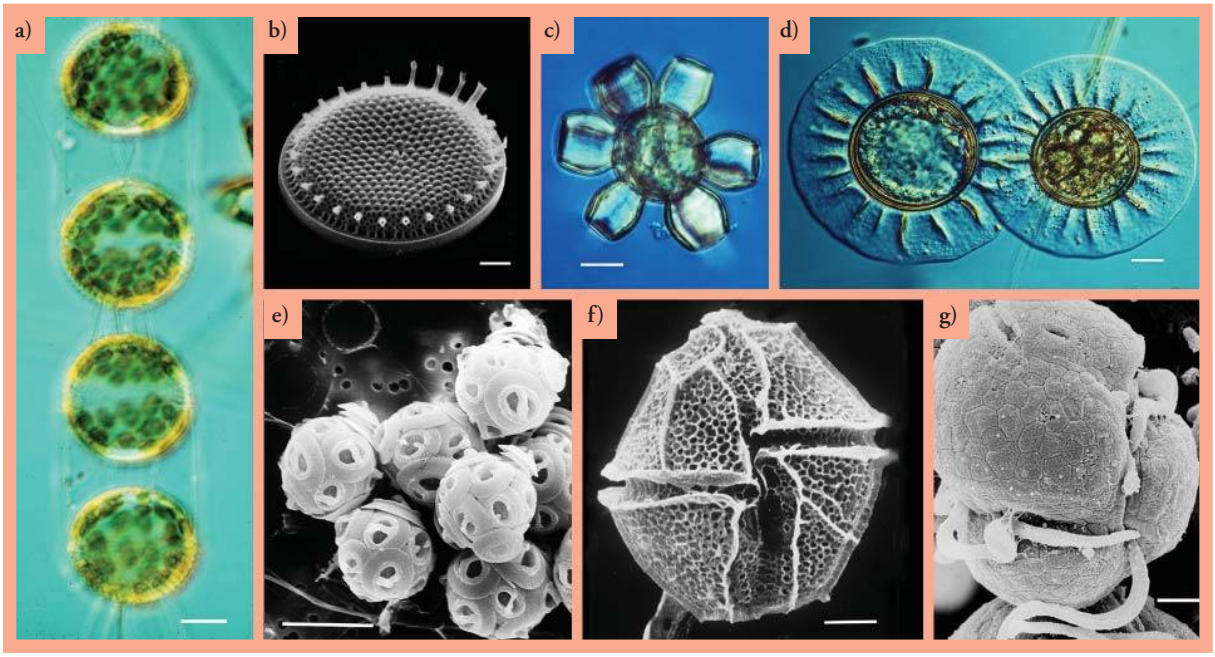

Figure 2 Examples of eukaryotic marine phytoplankton: light micrographs (Nomarski differential interference microscopy) of living cells, and scanning electron micrographs of dried and coated cells. **(a)** A chain of the diatom *Stephanopyxis nipponica.* **(b)** A single valve (half of the silicified cell wall) of the diatom *Thalassiosira pacifica.* **(c)** The large, tropical coccolithophore *Scyphosphaera apsteinii.* **(d)** An overlapping pair of phycomas of the prasinophyte *Pterosperma moebii.* **(e)** A clump of coccospheres of *Gephyrocapsa oceanica.* **(f)** The athecate ('naked') dinoflagellate *Karlodinium micrum* (= *Gyrodinium galatheanum*). **(g)** The thecate dinoflagellate *Lingulodinium polyedra* (flagella missing). Scale bars: (a,c,e.f) 10 µm; (b,g) 2 µm; (d) 25 µm.[1]

on the time scale of both evolutionary adaptation and short-term acclimation. Other publications synthesise the available information in this area in the context of the wider questions of determinants of marine primary productivity. One publication in which the senior author was involved was the Royal Society report on Ocean Acidification due to Increasing Atmospheric Carbon Dioxide.

Man's activities have released a large amount of carbon dioxide to the atmosphere over the last two centuries. A third of this carbon dioxide remains in the atmosphere as a contributor to the greenhouse effect, a third has been accumulated in terrestrial ecosystems, and the remaining third is now in the ocean. The ocean is thus responsible for the removal of half of the anthropogenic carbon dioxide that is not found in the atmosphere. Most of the carbon dioxide dissolving in the ocean remains in the form of inorganic carbon, but this does not mean that it has no biological effects. In particular, the changes to the equilibrium among the various chemical species of the inorganic carbon system and the associated lowering of pH decreases the degree of super-saturation of the surface ocean with respect to solid phases of calcium carbonate. This in turn decreases the potential for calcification of organisms; among the phytoplankton these calcified organisms are essentially all coccolithophores (Fig. 2), which are members of the Prymnesiophyceae (Fig. 1). Coccolithophores are quantitatively important members of the phytoplankton; while increased surface ocean carbon dioxide can reduce calcification by coccolithophores, it can increase the production of organic carbon in photosynthesis by these organisms. Work is continuing, here and in other laboratories, on the generality of the previously reported effects of increased carbon dioxide on coccolithophores.

References

[1] Falkowski, P.G., Katz, M.E., Knoll, A.H., Quigg, A., Raven, J.A., Schofield, O. & Taylor, F.J.R. (2004). *Science* **305**, 354-360.

Producing high-quality statistical software

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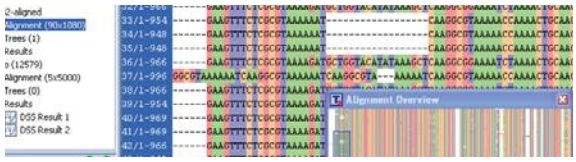


Biomathematics and Statistics Scotland

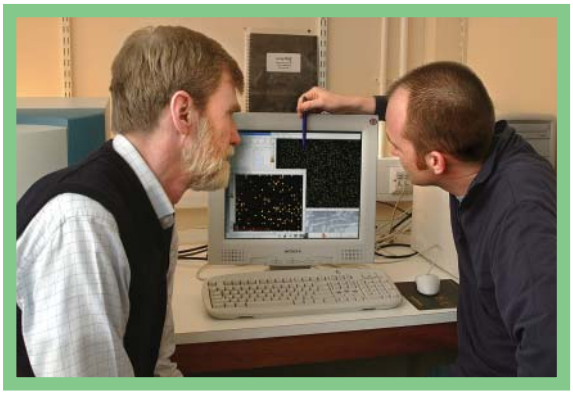
D.A. Elston

Biomathematics and Statistics Scotland (BioSS) holds a central position in SEERAD-sponsored research, with a cross-organisational role and emphasis on methodological issues. Formally, BioSS forms part of the SCRI family, with the distinctive remit:

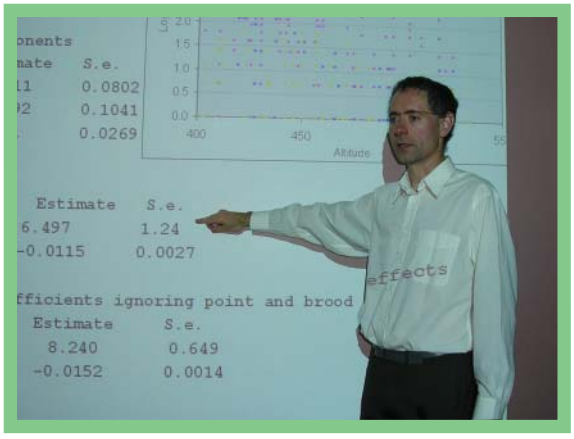
> *"to support the research programme of the Scottish Executive Environment and Rural Affairs Department and its sponsored institutes, through specialist advice and training, and to provide research in statistics and biomathematics."*

To achieve this remit, BioSS has a distributed staffing structure with headquarters on the King's Buildings science campus of the University of Edinburgh and offices at SEERAD-sponsored research organisations in Edinburgh, Aberdeen, Dundee and Ayr. The three main BioSS activities, namely research, consultancy and knowledge transfer, can be summarised as follows.

Research BioSS has an international reputation for its research in biomathematics and statistics. Our research is partitioned into three themes, each of which draws on the expertise and experience of staff: statistical genomics and bioinformatics; spatial and temporal models; process and systems modelling. BioSS also has many active links with universities and research organisations in Scotland, the rest of the UK and beyond.



Consultancy BioSS consultants add quantitative expertise to research throughout Scotland. Our staff have technical skills that are applicable to a wide range of scientific problems and the communication skills that allow them to interact effectively with scientists from other disciplines. Scientific areas in which we have particular expertise include: plant science; animal health and welfare; ecology and environmental science; human health and nutrition.



Knowledge Transfer BioSS bridges the gap between the development and application of biomathematics and statistics, and we are strongly committed to the dissemination of modern quantitative methods to the scientific community, government and the bio-industries. Key aspects of our programme of knowledge transfer include: development of software products; delivery of training courses for scientists; supervision of PhD students.

Producing high-quality statistical software

I. Milne, F. Wright, C. Hackett & J. McNicol

BioSS works at the interface between the development and application of quantitative methodologies. We are strongly committed to the dissemination of state of the art quantitative methods to a wide range of recipients, including the scientific community, research students, government and the bioindustries. Here we describe two user-friendly software applications produced for this purpose.

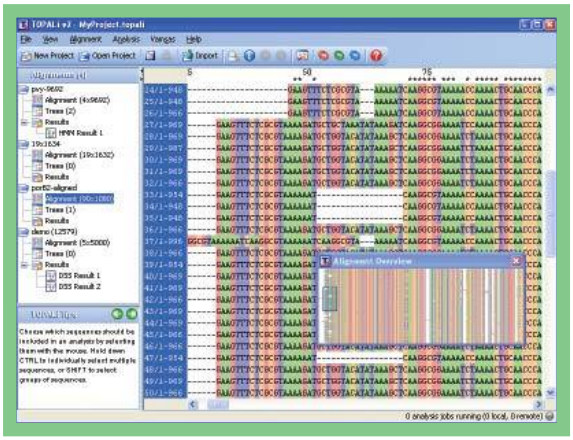


Figure 1 A 90seq by 1080bp DNA multiple alignment viewed in zoom and overview modes.

TOPALi (Fig. 1 and 2) Conventional phylogenetic tree estimation methods, applied to DNA multiple alignments, assume that all sites have the same evolutionary history. This assumption is violated if recombination has occurred among any sequences. Recombination produces mosaic sequences, which may cause errors in phylogenetic tree estimation. If recombination is possible, a check for mosaic sequences is essential prior to phylogenetic analysis.

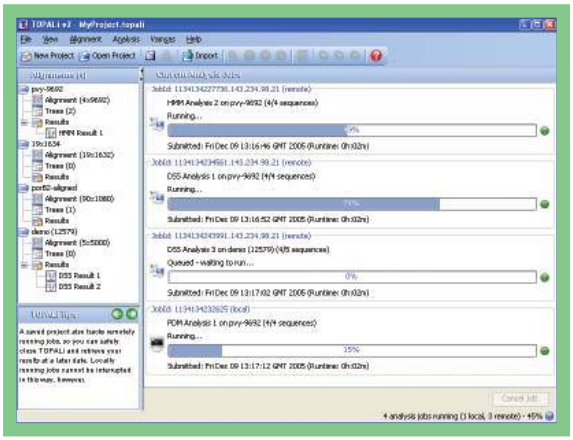


Figure 2 TOPALi allows for multiple analysis jobs to be run simultaneously on remote clusters.

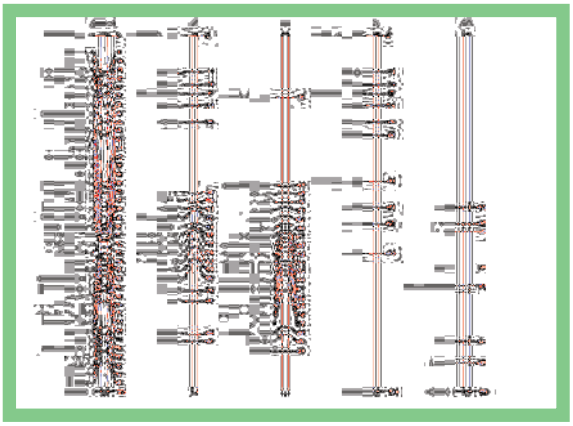


Figure 3 Linkage map of potato linkage group IV for the SCRI breeding clone 12601ab1.

Our software, TOPALi, provides an interface to three methods of recombination detection (Difference of Sums of Squares, Probabilistic Divergence Measures, and a Hidden Markov Model) that look for changes in phylogenetic tree topologies as we move a window along an alignment. These methods differ in the number of sequences that can be analysed and in their computational speed. TOPALi provides a complete graphical analysis tool for detecting recombinants in DNA multiple alignments. All tasks can be automated, requiring minimal user-intervention.

Recent development of TOPALi (in collaboration with the University of Dundee and the European Bio-

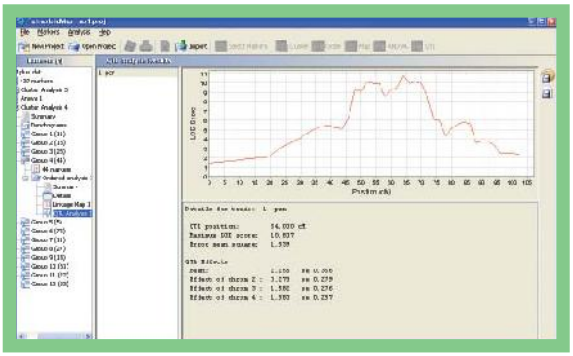
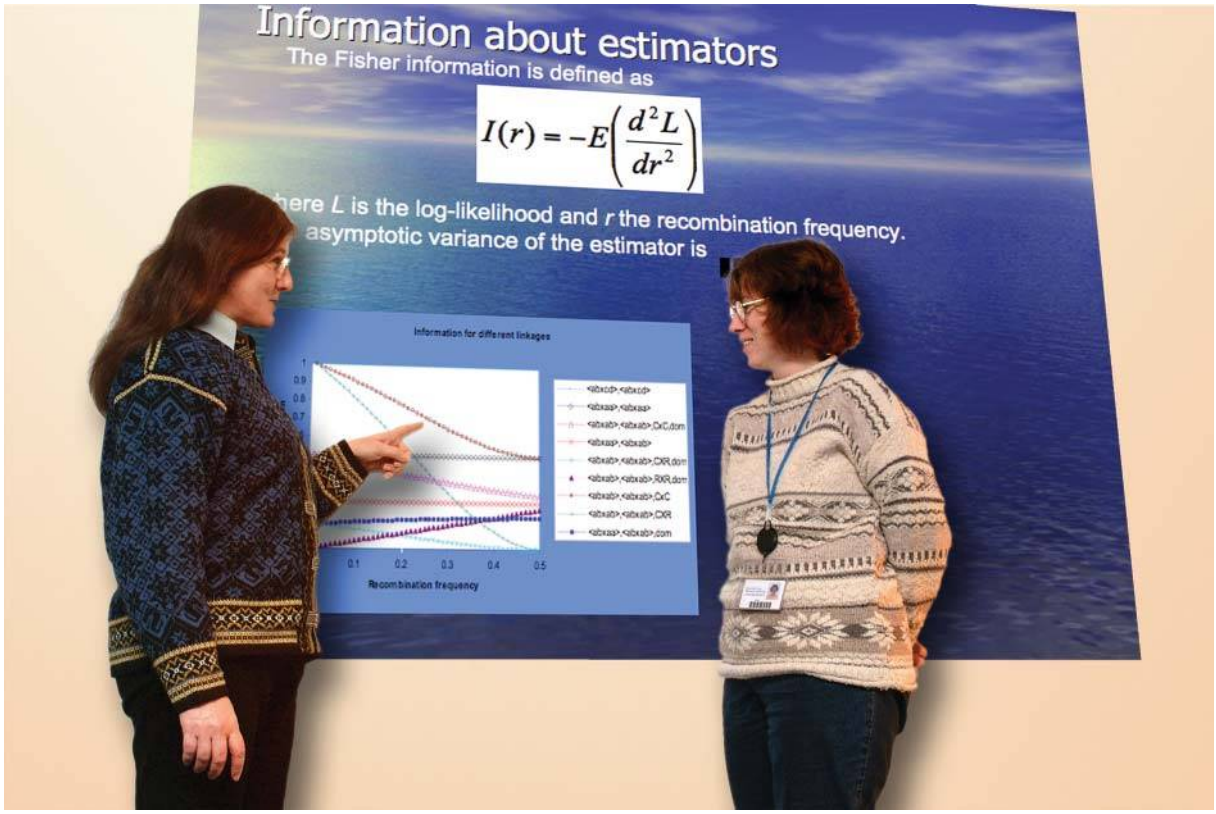


Figure 4 Lod profile for a QTL affecting PCN resistance on linkage group IV of 12601ab1.



informatics Institute in Cambridge) has concentrated on increasing its efficiency by programming many of its analyses for parallel computation, and accessing and running them via one or more high-performance computing clusters. As part of this work, new ways of interacting with the statistical programs running remotely have been designed, primarily through the use of web services. The ultimate goal is for the user to benefit from accessing distributed, high-performance facilities (such as the 28 CPU cluster at SCRI) from their normal desktop environment via a seamless high-quality graphical interface.

TetraploidMap (Fig. 3 and 4) The TetraploidMap program has been developed for calculating linkage maps and QTL mapping for autotetraploid species, such as potato. The program can be used to analyse both dominant and codominant markers scored for two parents and their offspring. Cluster analysis is used to separate the molecular markers into linkage groups. Recombination frequencies are calculated between all pairs of markers within a linkage group using the EM algorithm, and simulated annealing is used to order the markers.

Phenotypic traits, such as yield or disease levels, can be analysed by two methods. A simple marker regression method analyses each marker in turn to detect the markers that are most closely associated with the trait. Interval mapping can then be carried out for the linkage groups containing these markers to find the most likely QTL location and its mode of action (simplex, duplex, dominant etc.).

TetraploidMap is based on methodology developed by BioSS in collaboration with SCRI scientists since 1996, partly funded by a grant from the BBSRC GAIT initiative. It is also being used by groups in Europe and North and South America working on several autotetraploid species, including potato, leek and alfalfa.

Research services

Communication and Information Services The Communication team's key role is to support research and other support services to achieve the objectives of the Corporate Plan and to promote SCRI and its activities to a range of internal and external stakeholders. We arrange visits, conferences, exhibitions, events and undertake public relations work to raise awareness and understanding of SCRI's scientific research to industry, politicians, school children and the general public to name but a few. Our successes include the launch of the Living Field CD, distributed to every school in Scotland; industry events such as Potatoes in Practice; as well as many visits by students from school, college and university, farmers and special interest groups.

The Visual Aids team provides publicity material in the form of leaflets, publications, posters, exhibits and maintain the website to promote SCRI.

The Institute's Library is continuing to develop further and make available information from scientist's desktops. Subscriptions to electronic bibliographic databases and journals are increasing but there is still a substantial proportion of scientific literature in print which is not duplicated in electronic format that is housed in the Library.

Information Technology underpins all our computerised information systems, business processes and information requirements There are approx 500 PC's on site used as general purpose IT systems (email, word processing, etc.) and various networks and infrastructure to support and enhance the capability of our technology requirements. We recently installed a Storage Area Network (SAN) to further increase the data capacity and resilience of the system, including high capacity backup. Our internet connection is via FATMAN (Fife And Tayside Metropolitan Area Network) which in turn connects us to JANET (UK Joint Academic Network). A key responsibility for IT is in ensuring secure connections for all information transfer, and this is achieved by the use of firewalls, spam filtering, automated virus checking at all points and automatic patch delivery to systems. In addition to the responsibility for the running of the infrastructure and servers at the Institute, IT is involved in the development of web-enabled database applications and portal/workflow enhancements.

Finance and Administration The finance department consists of a small team of six people who provide financial support and advice to research and other activities of the Institute through planning, management, and control of its business operations.

A wide range of activities is undertaken which can be summarised as stewardship, input into the strategic

planning process, and transaction processing. There is, in addition, active participation in the Institute's risk assessment procedures.

The department is responsible for putting in place internal control systems that are suitable for the needs of the business and ensuring that these systems, and adherence to them, are reviewed by independent internal audit. The department's procedures aim to minimise the occurrence of fraud and misappropriation of funds, and the safeguarding of the assets of the Institute. In addition, current practices are continually reviewed to improve value for money.

The department works closely with research and support departments to develop strategic financial and operational plans and provides regular updated forecasts to support decision making processes.

The finance department is responsible for producing financial accounts, including the annual statutory accounts, which comply with current statutory and regulatory obligations, and also aims to produce accurate, timely and meaningful management information to enable Institute management to monitor performance against budgets.

The department endeavours to ensure that all income due to the Institute is recorded and received timeously, and that payments to suppliers are accurately made in accordance with targets and guidelines.

Human Resources The 4 members of the HR Team provide support to the managers and staff at SCRI helping them to lead and develop staff effectively and by ensuring fair and effective recruitment and induction of the 31 staff who started work at SCRI in 2004/2005. HR also encourages staff to take advantage of the wide range of development opportunities offered with 52% of the staff taking part in formal training events and 21 staff achieving promotion during 2004/2005. The HR team is also responsible for ensuring the development and implementation of appropriate polices to reward staff effectively which included the introduction of a childcare vouchers scheme as well as ensuring that SCRI was successfully reaccredited as an Investors in People organisation in 2005.

Health and Safety, Quality Assurance and Environmental Management Auditing within the three disciplines intensified this year. Adding to certification under the international Quality Assurance standard ISO9001:2000, SCRI and MRS were awarded certificates for compliance with the Environmental Management standard ISO14001:2004 in spring 2005. Thanks are due to Scottish Enterprise Tayside for meeting fifty per cent of the cost of the pre-audit consultations. In autumn, the SCRI group was subjected to its first integrated management system audit examining all three disciplines together. The outcome was that health and safety management was certified compliant with the standard OHSAS 18001, complementing the other two certified systems.

SCRI was also awarded the Scotland's Health at Work (SHAW) Bronze award in May 2005. In addition, a Business Continuity Plan has been produced and exercised.

Risk Management is overseen by the Audit Committee of the Governing Body, the Institute Director, the Institute Secretary, the Institute Deputy Director of Finance and Administration, the Institute Engineer and the Institute Health and Safety Co-ordinator. Other members of Institute staff may be co-opted as required. The remit of the Risk Committee includes ensuring the implementation of the Institute's risk policy, ensuring that the Institute has a reliable and comprehensive system of internal control and risk management, and encouraging the development of a culture of risk awareness and risk management in all staff.

The Committee is required to review all aspects of risk management, at least annually, to report to the

Governing Body upon the efficacy of such systems and to advise the Governing Body upon the Institute's risk policy.

The Committee ensures that the Institute has a comprehensive system of internal control and risk training, determines the principal areas of risk, their likelihood and exposure, in particular those related to the operations and finances of the business, and are satisfied that controls and systems are in place to mitigate the company's exposure to the major risks.

Engineering & Maintenance Department Extensive laboratory administration and ancillary facilities are maintained by the Engineering department who are also responsible for electrical, heating, plumbing, data/telephony cabling, painting and joinery work. In addition, major building work undertaken by subcontractors is supervised by the department.

Equipment and instrumentation continues to become increasingly sophisticated and the Institute's engineers aquire new skills to adapt to the increasing demands.

The Institute operates from a site with disparate buildings housing administrative offices, research facilities and storage areas for scientific and farm equipment and plant material including the Commonwealth Potato Collection. The engineering department, in addition to maintaining the estate's building stock, is also responsible for carrying out a programme of refurbishment which continually upgrades laboratories and administrative offices.

Utilities costs are a significant component of the running costs of the Institute and measures have been taken to reduce the Institute's consumption of energy and further efficiency gains will be sought. The Engineering & Maintenance Department also undertakes routine maintenance and repairs to scientific equipment to restrict costs.

The department, through its farm workshop, provides a repair and maintenance service to the Institute's fleet of tractors and agricultural machinery.

Estate, Glasshouse and Field Services Among the facilities which distinguish the Institute from other organisations is a comprehensive range of glasshouse and controlled-environment cabinets and rooms. There are approximately 10,000 m² of glasshouse facility available, ranging from cold glasshouses to sophisticated containment glasshouses with associated laboratories. In addition, the Institute has 13,000 m² of polytunnels and net structures. Twenty five staff

service the demand from scientists throughout the year and are responsible for the production of consistent, high quality, plant material under a large variety of experimental regimes. The provision of these facilities is made possible as a result of capital grant from the Scottish Executive Environment and Rural Affairs Department. The Institute has a meteorological site where data are collected for use by the Meteorological Office, SCRI scientists and the local community.

The Institute also has available approximately 172 ha of farmland on which to conduct a wide range of agricultural, horticultural and environmental trials. An expert service is provided in relation to land preparation, sowing, drilling, harvest and clearance of residues. In addition to being responsible for the production of annual crops such as potatoes, brassicas and cereals, field staff also maintain the Institute's 10 ha of perennial soft fruit trials.

The Institute is a LEAF Innovation Centre and a series of display boards on food webs, beneficial organisms and pests has been erected at strategic points within the Institute as part of the Invergowrie Path Network initiative.

A 0.15 ha site has been developed into an educational resource aimed at the local community and schools, and the Living Field Community Garden will show the links between science, agriculture and the environment by the use of demonstration plots, interactive exhibits and information boards.

Various projects under the Countryside Premium Scheme were continued and extended, including tree wind-breaks, species-rich grassland, beetle banks and mixed native hedgerows. The presentation of experi-

ments has been improved by the grassing of field roadways, reducing the need for herbicide sprays and enhancing the biodiversity within the grass sward.

Trials on minimum tillage and soil disturbance continue.

The Staff Association has been very active providing social events for all staff and raising money through many events for nominated charities.

The larger events held during 2004/5 were a Christmas disco, lunch, fayre, and children's parties. In June, the Association holds a summer barbecue with an average of 250 staff, family and friends in attendance. Two quiz nights were held in the Fort Hotel in Broughty Ferry. In November 2005, an Institute ceilidh was revived after an absence of several years, and over 100 people attended. Other events that took place included a bowling/zap-zone night, and hill walking. Blood donor sessions are arranged several times a year and are coordinated to allow staff time to attend. The Association gives support to the golf, fishing, and football fraternities along with Corporate Sports membership at Dundee University, and Yoga and Tai Chi sessions. Three new activities have recently started – Egyptian belly dance, Keep fit, and Salsa.

Member's benefits include entry into a monthly draw to win meal and cinema vouchers. There are use of National Trust corporate admission cards, a Booker cash and carry card, subsidies to reduce costs of the Christmas lunch in the canteen, fresh cut trees and children's parties. *Which* magazine is provided in the SCRI library and is available for online access. The office bearers and committee are elected annually at the AGM where members are encouraged to nominate both local and national charities to be beneficiaries of the funds raised throughout the year. In 2004, five charities received £225 each. They were Rachel House Children's Hospice, Fife, Riding for the Disabled Association, National Asthma Campaign, Neurosurgical Ward 23B at Ninewells Hospital, and Advocating Together. For 2005, three charities will receive £340 each. They are, Dundee Blind & Partially Sighted, Dundee Women's Aid, and Menzieshill Community Centre.

The Staff Association remains an integral part of SCRI, as it contributes greatly to the corporate well being and was instrumental in helping SCRI gain a "Bronze" award status with Scotland Health at Work Initiative (SHAW).

Scottish Society for Crop Research

W.H. Macfarlane Smith

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

Membership Numbers:- 221

The Scottish Society for Crop Research is a registered Friendly Society, formed in 1981 by the amalgamation of the Scottish Society for Research in Plant Breeding and the Scottish Horticultural Research Association.

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

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

The Society continues to support research work on wheat blends and low input production, and the production of a soft fruit pathogen database. Work on a quantitative detection method for potato cyst nematode is being funded and financial support provided for a speaker at the Crop Protection Northern Britain Conference. Ongoing support is being provided for the consortium producing new varieties of raspberry and will continue until 2009.

The Annual General Meeting was held on 24th May 2005, after which the SSCR Lecture was given by Professor Peter Gregory, Director of SCRI, entitled 'Sustainable Agriculture – Local and International Perspectives'.

The re-incarnation of the old cereal walk, now entitled 'Cereal Solutions', was held on 1st July 2005 and attracted 40 visitors.

The Fruit for the Future event was held on 14th July 2005, and attracted 30 breeders, growers, end-users and processors who were keen to see the latest research on raspberries, strawberries, blackcurrants and other soft fruits. Prospective new varieties of raspberry and strawberry were available for tasting assessment.

'Potatoes in Practice', the potato event supported by the Society, the British Potato Council, the Scottish Agricultural College, CSC Crop Protection Ltd., and the Scottish Crop Research Institute, was held on 11th

August 2005. The event attracted almost 500 visitors, the highest number to attend this event so far. It is now recognized as the predominant outdoor potato event in the UK.

The Crop Sub-Committees held other meetings during the year to provide information to their relevant industries, and to prioritize proposed research for approval and funding by the Committee of Management.

The Society membership has increased by 5% in the last year. As a further means of boosting membership, additional activities, such as visits to processors, are now taking place and life membership at £100 is available.

The Committee of Management is keen to encourage growers and processors to join the Society and to participate not just in the various crop-based meetings but also in the management of the Society and its various Sub-Committees.

A new colour version of the Society Newsletter was produced early in 2005 and was well received. A new Society Website is now on line, and it is hoped that this will be the main conduit for information to Society members in the future. The first part of the Web site is freely available but subsequent sections are password-protected for access by Society members only.

Mylnefield Research Services (MRS)

N.W. Kerby & J.B. Snape

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

To develop commercially the Scottish Crop Research Institute's scientific expertise, resources and intellectual property, and to improve the quality of services to achieve new standards of excellence.

Finances The income of MRS increased to £1.91 million in 2004/2005, an increase of almost 15% on the previous year. MRS transferred £1.3 million to the SCRI Group, including £132k of Gift Aid. As in previous years, contract research (72%) was the biggest contributor to income, followed by royalties (12%) and analytical services (10%).

Licensing and IP Asset Management MRS is responsible for ensuring that all varieties emanating from breeding programmes at SCRI are protected by plant variety rights, drawing up license agreements with third parties and collecting the royalties. MRS licences potatoes, forage and salad rape, turnip, kale, blackcurrants, blackberry, raspberry and strawberry varieties and currently has a portfolio of 470 licences in 18 countries.

Since 1st April 2004, two potato varieties and one kale variety have been added to the UK National List and another five potato varieties have been submitted to National List trials. Three potato varieties and one kale variety were granted EU Plant Variety Rights. In addition there were nine applications for Plant Variety Rights for potato varieties, including five in Australia. SCRI varieties are being trialled all over the world including Japan (potatoes), China (soft fruit), Romania (soft fruit and potatoes), Australia (potatoes), Cuba (potatoes) and Egypt (potatoes).

Proof of Concept Projects MRS is responsible for commercialising the output of Proof of Concept projects funded by Scottish Enterprise at SCRI. Current projects include a novel method of producing ascorbic acid in yeast (Roberto Viola and Rob Hancock), the development of a service to screen genes for nematicidal, fungicidal and insecticidal activitity (John Jones and Sean Chapman), a new method for analysing the physical and chemical properties of timber (Derek Stewart) and the development of environmental molecular diagnostics for water quality assessment (Tim Daniell). Discussions with commercial companies are on-going regarding licensing these technologies and / or establishing new businesses based at SCRI.

Mylnefield Lipid Analysis The lipid analysis business was rebranded as Mylnefield Lipid Analysis and increased emphasis placed on marketing services. This has resulted in an increase in turnover and winning a significant contract with a multi-national pharmaceutical company. Further investment in equipment, notably stability cabinets and an additional gas chromatograph, has enabled us to significantly grow the business.

Developing Markets In May 2005, MRS led an Agricultural Trade Mission, organised by China Britain Business Council (CBBC), to China and continued to concentrate its efforts on China lifting the import ban on UK seed potatoes. A significant opportunity exists to both MRS and SCRI, in helping China develop its potato industry. SCRI and MRS presented papers at, and co-organised the International Potato Symposium in Sichuan, where the UK was very well represented.

Following discussion between MRS, CBBC and Defra, potato projects are being prioritised as an industry

need for funding under the new Memorandum of Understanding between Defra and the Ministry of Agriculture of the People's Republic of China.

Nigel Kerby was appointed to the Board of CBBC and, in his capacity as a Board Member, was invited to meet President Hu Jintau on his state visit to the UK.

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

Prof. John Hillman, Prof. Richard Cogdell and Mr Ed Angus all stepped down from the MRS Board of Directors after many years services. We welcome Prof. Peter Gregory to the Board.

Knowledge Transfer and Exploitation (KTE) MRS plays an integral role in the overall knowledge transfer strategy of SCRI. In summer 2005, MRS contacted more than 250 stakeholders for feedback on the new SEERAD-funded work packages and had numerous follow-on discussions. In addition, MRS contributed to the 'Programme for Knowledge Management and Transfer to Deliver SEERAD's Strategy for Research on the Environment, Biology and Agriculture'- the overarching strategy for knowledge transfer. We have also been proactive in disseminating information on SCRI to a wide range of end-users, and gave 9 invited presentations at national and international conferences and symposia.

Chinese Administration for Quality Supervision, Inspection and Quarantine (AQSIQ) visit SCRI (June 2004)

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 valuable time without recompense.

Mylnefield Trust and Mylnefield Holdings

The Mylnefield Trust and Mylnefield Holdings Ltd. (MHL) were established in 2000 in order to give the SCRI Group the flexibility it requires to grow. Central to this growth is the creation of a number of spin-out companies, such as Scottish Potato Technology Ltd, in which MHL on behalf of the SCRI Group, will hold equity.

The Trustees are a group of individuals, including several members of the MRS Board of Directors and the SCRI Governing Body. The Trust currently has funds of approximately £300K, achieved mainly through donations from MRS Ltd.

The Trust has charitable status and has as its prime objectives:

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

A Local Art-Science Collaboration

To date the Trust has funded:

- An Incentive Fund to provide further support for scientists actively winning external contracts to pursue scientific research
- Funds to support the establishment of an Education Officer at SCRI
- A hardship fund for an overseas student
- Start-up funding for the Product Innovation Centre
- In 2004 The Mylnefield Trust funded 6 projects totalling £21,349

During the financial year 2005-06 The Mylnefield Trust is supporting 5 projects (detailed below) amounting to £19,850. Also during this financial year, The Mylnefield Trust is supporting scientific publications up to a value of £10,000.

Name	Title	Value
Tim Daniell/Jen Kennedy	Re-colonisation Dynamics of Arbuscular Mycorrhizal Fungi	£3,050
Hugh Barker/Mark Petrie/Bruce Marshall	Development of Interactive Web-Based Applications to Provide Information on Soft Fruit Pests and Pathogens	£5,800
Sharon Neilson	Living Field Community Garden	£3,500
John Brown/Dave Marshall	Development of Portal System for Plant Science Scotland	£2,500
Ian Toth/Leighton Pritchard	Bringing Plant Science Closer to the Public: A Local Art-Science Collaboration	£5,000

Publications

Publications for the year 2004 and 2005 are classified in the following manner:

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

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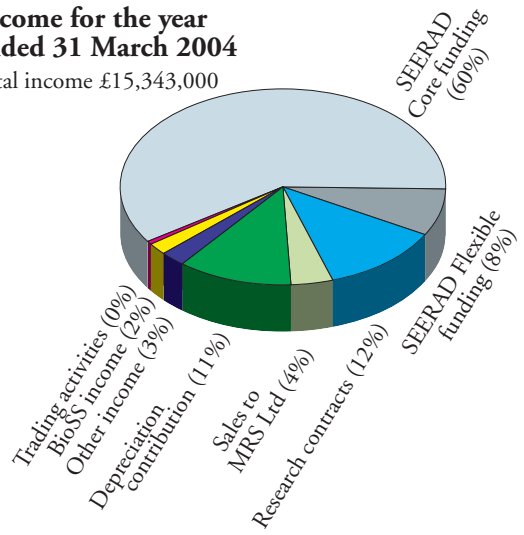
Summary of the Accounts

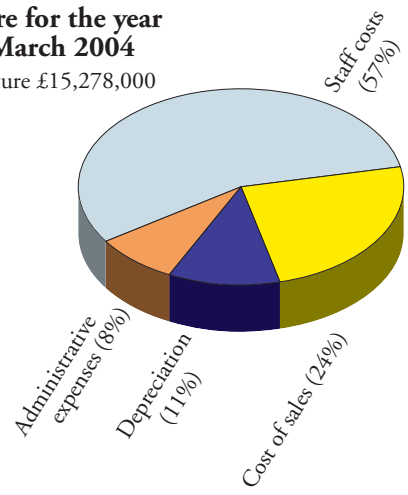
Income for the year ended 31 March 2004

Total income £15,343,000



Expenditure for the year ended 31 March 2004

Total expenditure £15,278,000



Balance sheet at 31 March 2004 Total value £27,223,000

Assets

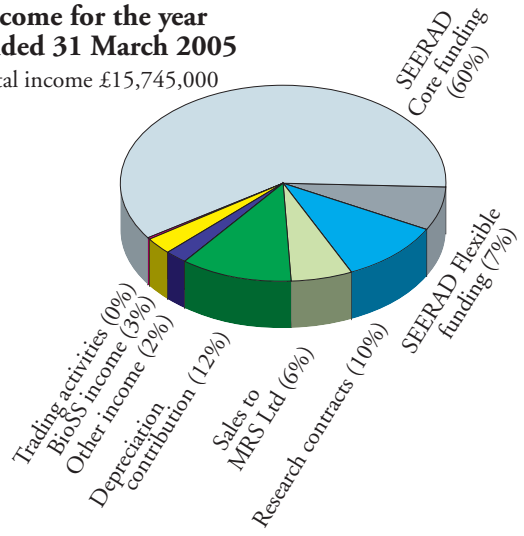
Fixed assets	95 %
Stocks	0 %
Debtors	5 %

Liabilities

Capital reserve	87 %
Income & expenditure account	2 %
Current liabilities	11 %

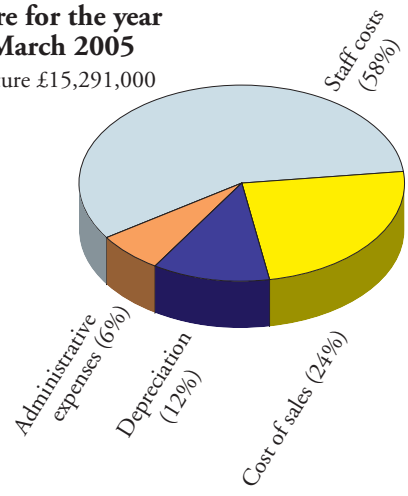
Income for the year ended 31 March 2005

Total income £15,745,000



Expenditure for the year ended 31 March 2005

Total expenditure £15,291,000



Balance sheet at 31 March 2005 Total value £28,802,000

Assets

Fixed assets	94 %
Stocks	0 %
Debtors	6 %

Liabilities

Capital reserve	86 %
Income & expenditure account	4 %
Current liabilities	10 %

Distinctions & Awards

January 2005 Alf Low MBE.

May 2004 Konstantina Stamati and Marcelo de Oliveira winners of the SCRI heat of the SABRI postgraduate competition.

June 2004 Jim Mason is presented with the Royal Highland and Agricultural Society of Scotland long service award by Mr Allan Wilson MSP, Deputy Minister for Environment and Rural Affairs.

June 2004 Marcelo de Oliveira wins the SABRI Postgraduate Competition and is presented with his prize by Professor M S Swaminathan FRS.

July 2004 Dr Tim Daniell Proof of Concept award. This project has received financial assistance from the Proof of Concept Fund managed by Scottish Enterprise and the Scottish Executive. The Proof of Concept Fund supports the pre-commercialisation of leading-edge technologies emerging from Scotland's Universities, Research Institutes and NHS Trusts.

August 2004 Presentation of the Peter Massalski Prize to Dr Steve Whisson by SSCR Chair John Whitehead.

September 2004 Living Field Garden Stand won Silver medal at Dundee Flower and Food festival.

October 2004 Scotia Agricultural Club awards for postgraduate studies: Sanjeev Kumar Sharma, Marcelo de Oliveira and Laurence Ducreux.

October 2004 Name the Swede Prizewinner Rory Lawson (12) gets his prize for "Gowrie".

November 2004 Dr Hardie memorial award from the VTSC Growers Association to Donald MacKerron for his work of 33 years at SCRI presented at the BPC Conference in Crieff.

Februry 2005 Prof. Frank Gunstone receives the Alton E. Bailey Award from the American Oil Chemists Society in recognition of his outstanding research and exceptional contribution to the oils and fats field.

May 2005 SHAW Bronze award photo courtesy of the Evening Telegraph showing Mike De,Maine and Kristy Grant (back row).

October 2005 John Brown made Honorary Professor at the University of Dundee

Higher Degrees

Nawsheen Taleb. 2004 PhD University of Mauritius. Determination of the molecular basis of genetic resistance to *Phytophthora infestans* in potato.

Rodanthi Holeva. 2004 PhD University of Dundee. Molecular differentiation of trichodorid nematodes and functional studies of the transmission of their associated *Tobacco rattle virus.*

Cleber Furlanetto. 2004 PhD University of Glasgow. Analysis of secreted proteins from the ectoparasitic nematode *Xiphinema index.*

Claudio Marcelo de Oliveira. 2004 PhD University of Dundee. Genetic and morphological diversity of longidorid nematodes from Brazil.

Jafar Bolandandam. 2005 PhD University of Dundee. Studies on natural and transgenic host resistance to *Potato leafroll virus* and its aphid transmission.

Eleanor Gilroy. 2005 PhD University of Edinburgh. The role of plant defence genes in the hypersensitive response.

Alison Blake. 2005 MSc University of Dundee. Metabolic profiling for the chemotaxonomy of pleurocarpous mosses.

Yousuf Akhond. 2005 PhD University of Dundee. Biolistic DNA delivery into tobacco male gametophytes and its consequences.

Staff list as at 1 October 2005

Director P J Gregory BSc PhD Hon Dr (Debrecen) CBiol FIBiol FRASE[12,13,14,15]
Director of Science Co-ordination H V Davies BSc PhD CBiol FIBiol[1,2]
Director of Finance and Administration N G Hattersley BSc PhD ACMA

Genetics

R Waugh BSc PhD [3] *(Programme Leader)*
J Alexander BSc
S F Blackie BSc
N Bonar HNC
A Booth HNC
C Booth BSc
J E Bradshaw MA MSc PhD [3]
R M Brennan BSc PhD
J Brown
J W S Brown BSc PhD [3]
G J Bryan BSc PhD
G P Clark HNC BSc
M F B Dale BSc PhD [3]
D Davidson
L Donnelly
A Druka MSc PhD
B P Forster BSc PhD [3]
J D Fuller
S L Gordon HNC
J Graham BSc PhD
B Harrower HND BSc MSc
Y Hashim BSc PhD
P Hedley BSc PhD
I Hein MSc PhD
L Jorgensen HND
C Julia
R Keith NEBS
S H Kim BSc PhD
D P King BSc
D J Leader BSc PhD
D Lewandowska BSc
M S Liney HND
J Liu BSc MSc PhD
D C Lloyd BSc MSc
J Lyon
M Macaulay HNC BSc
S A MacFarlane BSc PhD
D F Marshall BSc PhD
H A Mathews
N McCallum BSc
S McCallum HNC NC HND BSc
G McKenzie HND BSc
K McLean BSc
J McNicoll HNC BSc
J Middlefell-Williams HNC
L G Milne BSc PhD
J Morris HND BSc
S Mudie BSc
M Myles ONC
D Nwankwo BSc MSc
G Ramsay BSc PhD
L Ramsay BSc PhD
N Rostoks BSc MSc PhD
J Russell BSc PhD
P D Shaw MSc
C G Simpson BSc PhD
G G Simpson BSc PhD
K Smith DipHE
P L Smith BSc
G E L Swan
M M Swanson BSc PhD
J S Swanston BSc PhD CBiol MIBiol
W T B Thomas BSc PhD
I M Tierney BSc MSc
D Todd BSc MSc
G Wilde
S L Williamson BSc
R N Wilson HNC
M Winfield BSc PhD
M R Woodhead BSc PhD
G R Young HNC

Dundee University Group 1
A J Flavell BSc PhD *(Group Leader)*
R Jing BSc PhD
J Lee BSc PhD
M Lyons BSc
N H Syed BSc PhD

Dundee University Group 2
C Halpin BSc MSc HDip PhD *(Group Leader)*
A Barakate BSc PhD
E Douglas BSc
A Goldie BSc
S Haupt BSc PhD
J Searle BSc
J Stephens BSc PhD

Mylnefield Research Services
D Coyle
G Duncan
L Ferguson
S N Jennings BSc
G Reid

Plant Pathology

L Torrance BSc PhD [3] *(Programme Leader)*
M Armstrong BSc PhD
A O Avrova BSc PhD
S Bagirova BSc PhD
H Barker BSc PhD [3]
K Bell BSc PhD
P R J Birch BSc PhD
V C Blok BSc MSc PhD
P Boevink BSc PhD
J L Brierley BSc PhD
W Burry
M Burton
T Canto BSc PhD
F Carr ONC HND
L M Castelli BSc MSc PhD
S N Chapman BSc PhD
D E L Cooke BSc PhD
G H Cowan HNC MSc
A Dolan HNC
B Fenton BSc PhD CBiol MIBiol [3]
G L Fraser
T L Gillespie BSc PhD
E Gilroy BSc PhD
S C Gordon HNC [3]
D C Guy HND
J Heilbronn HNC BSc PhD
A M Holt
S N Humphris HNC BSc PhD
L J Hyman BA MSc
K Jackson BSc
J T Jones BSc PhD [3]
A Kumar BSc PhD
C Lacomme BSc PhD
S S Lamond
M J M Latijnhouwers BSc PhD
A K Lees BSc PhD
H Liu BSc MSc
G D Lyon BSc MSc DIC PhD [3]
G L Malloch DCR BSc PhD
L Mazzitelli BSc
W J McGavin BSc
K D McGeachy HNC
J McMillan
A C Newton BSc PhD
P F Palukaitis BSc PhD [1,5,10]
A J Paterson HND
M S Phillips BSc [3]
Y Pitkin BTec HND
K S Pradel BSc PhD
L Pritchard BSc PhD
E F O Randall MSc PhD
B Reavy BSc D Phil
W Ridley
A G Roberts BSc PhD [3]
L Shang BSc
J Shaw BSc
A Smith BSc
R M Solomon-Blackburn BA MSc
J N Squires BSc PhD
J A Stewart HND BSc
L Sullivan BSc
M Talianski PhD DSc [11]
I K Toth BSc PhD [6]
E Warden ONC
S Whisson BSc PhD
N A Williams HNC
A C M Winfield BSc
K M Wright MA PhD
K Wypijewski MSc 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 Lecturer, 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

Quality Health & Nutrition

D Stewart BSc PhD *(Programme Leader)*
M G Anderson MSc BSc
R G Campbell BSc
S C Conner BSc MSc CChem MRSC
H V Davies BSc PhD CBiol FIBiol [1,2]
G Dobson BSc PhD
P M Dobson
L J M Ducreux BSc MSc MPhil
A Emslie BSc MSc
F Falconer HNC
S M Glidewell MA MSc PhD
D W Griffiths MA PhD CChem MRSC
R D Hancock BSc PhD
R Hutchison
G J McDougall BSc PhD
D McRae ONC
W L Morris BSc MSc
P Neave
S D A Pont BSc
H A Ross HNC PhD CBiol MIBiol
L V T Shepherd BSc MSc PhD
T Shepherd BSc PhD
J A Sungurtas HND
M A Taylor BSc PhD [3,4]
S R Verrall HNC
P G Walker HND
J F Wilkie

Mylnefield Research Services
W C Christie MBE BSc PhD DSc CChem FRSE FRSC
C Fernie BSc
F Gunstone BSc PhD DSc FRSC FRSE CChem
L Hunter
R Razzo
S Rowbottom ONC HNC
C Traynor BSc
K Wood

Environment Plant Interactions

B Marshall BSc PhD ARCS [7] *(Interim Programme Leader)*
G Banks BSc MSc
G S Begg BSc PhD
A G Bengough BSc PhD[3]
K Binnie BSc
A N E Birch BSc PhD CBiol MIBiol FRES
L K Brown BSc
S Caul HNC
D Cullen BSc PhD
T J Daniell BSc PhD [3]
J Davidson BSc
M J Elliott BSc
L Ford BA
D C Gordon HNC
B S Griffiths BSc PhD [3]
P D Hallett BSc PhD
J Hans BSc MSc PhD
C Hawes BSc PhD
P P M Iannetta BSc PhD
S N Johnson BSc D Phil
A J Karley BA PhD
H L Kuan BSc MSc
J McCluskey BSc
B M McKenzie BSc PhD
S M Mitchell BSc
R Neilson HNC MSc PhD
A Parish BSc
S Regan BSc MSc
D M Roberts HND BSc PhD
G Robertson
C M Scrimgeour BSc PhD [3]
G R Squire BA PhD
W M Stein HNC BSc
J A Thompson BSc
T Valentine BSc PhD
R E Wheatley BSc PhD
J Wishart BSc PhD
G M Wright HNC
M Young HND MSc DipIT

Dundee University Group 3
H G Jones MA PhD FIHort *(Group Leader)*
I Leinonen PhD
R McLaren
R Ramsey BSc PhD
L Spencer BSc

Dundee University Group 4
J A Raven PhD FRSE FRS *(Group Leader)*
K Brown PhD
A Donald
F Lang
M MacKay MRes
M L McDowell
M Marconi
D R Ross
S Sobhy

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S E Stephens BSc MA MCLIP
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U M McKean MA DipLib
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S J Neilson DipBiolSci DipPollCon BSc
D Third
S K Thomson HND BA

Information Technology

S Clark HNC MSc *(Head of IT)*
L H Davidson BA
P J R Grimmond BA
R McCreary BSc
L A McGregor BSc
M Petrie BSc
P Smith BSc

Finance & Administration

N G Hattersley BSc PhD ACMA
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A Addison
S Bell
A J Cartwright BA DMS MCIPD
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R G Davidson
P Duncan
S Forsyth
K L Grant BA
B V Gunn
S Inglis
J Keith
L MacDonald BA CA
K Muir
M Murray
A Pack BA
W Patterson HND
M Pearson BSc
S M Phillip
S Smart
E L Stewart

Engineering & Maintenance

S Petrie BSc *(Head of E&M)*
J Anderson
D Byrne
C Conejo
R Craik
G J E Ewart
J Flight
A G Fox
D Gray HNC
K A Henry
E Lawrence
A Low
R D McLean
I C McNaughton HNC
E Millar
C G Milne
G Pugh
D J Redford
G C Roberts
D L K Robertson
J Rowe
W Scott
B Semple
M J Soutar
B Ward
R White

Estate Glasshouse & Field Services

P A Gill HND NEBOSH *(EGFS Manager)*
J Abernethy
P Baird
R Balfour
J R K Bennett
J T Bennett
E Caldwell
C A Cuthill NC
A G Dobson HNC HND
B Fleming
I Fleming
J M Ford
A C Fuller
M A Grassie HNC BEd
D J Harkins
P Heffell ONC
J Mason
T A Mason NEBSM
D I Matthew BSc
R McHutchon
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
H Wilson

Biomathematics and Statistics Scotland

Director of BioSS D A Elston BA MSc PhD

King's Buildings, University of Edinburgh
C A Glasbey MA DipMathStats PhD DSc MISI [7,8,9] *(Head of group)*
S M Bierman BSc MSc
A Butler BSc PhD
J B Coe MPhys PhD
J M Dickson BSc
D Glancy
E M Heyburn MA
D Husmeier BSc PhD
M A M Kirkwood DA
K Lin BSc PhD
A D Mann BSc
G R Marion BSc MSc PhD
I J McKendrick BSc PhD
I M Nevison MA
A M I Roberts BSc MSc
J Sales BSc MSc

West of Scotland Unit,
Hannah Research Institute
S Brocklehurst BSc PhD *(Head of group)*

Environmental Modelling Unit,
The Macaulay Institute
D A Elston BA MSc PhD *(Head of group)*
M J Brewer BSc PhD
E I Duff BSc
J M Potts BSc MSc PhD
D M Walker BSc MSc PhD

Aberdeen Unit,
Rowett Research Institute
G W Horgan BA MSc PhD *(Head of group)*
G Holtrop MSc PhD
C D Mayer MSc PhD

Dundee Unit,
Scottish Crop Research Institute
J W McNicol BSc MSc [3] *(Head of group)*
C A Hackett BA DipMathStats PhD
K M MacKenzie BSc MSc PhD
N Massat MRes MSc PhD
I R Milne BSc PhD
F G Wright BSc MSc PhD

Short-term visiting workers

Name	Country of origin	Programme	Month/yr of arrival	Length of stay
N Ahmad	UK	GEN	May-04	3 months
K Angelis	Czech	PP	Oct-04	3 weeks
N Archer	UK	PP	Feb-05	1 month
A Askarianzadeh	Iran	PP	Mar-05	6 months
G Axelsen	Norway	PP	Sep-05	8 months
J Bakonyi	Hungary	PP	Oct-05	1 month
K Bannon	UK	QHN	Jul-04	3 weeks
E Barker	UK	QHN	Jul-04	3 weeks
M Barre	France	PP	Sep-05	3 months
I Bayakev	Bulgaria	GEN	May-05	3 weeks
F Benites	Brazil	GEN	Jul-05	1 month
A Blanchard	France	PP	May-04	2 weeks
P Boisson	France	EPI	Feb-05	5 months
J Calcutt	UK	PP	Jul-04	2 months
A Chimento	Italy	PP	Apr-04	3 months
S Chittiboyina	UK	GEN	May-05	5 months
A Custodio	Portugal	PP	Aug-05	5 months
A Fadeev	Russia	PP	Jun-04	8 months
J Franckowiak	Canada	GEN	May-05	4 months
M Geraghty	UK	QHN	Oct-04	3 months
S G Gonzalez	Spain	GEN	Sep-04	3 months
A Gow	UK	QHN	Jul-04	3 weeks
E Grenier	France	PP	Apr-04	1 month
T Hamalainen	Finland	PP	May-04	3 months
R Hay	UK	PP	Sep-05	6 months
B Hinojosa	Spain	EPI	Jul-04	3 months
L Iggy	UK	GEN	Sep-05	4 months
S Janakowski	Poland	PP	Jun-04	3 months
E Jasinka	Germany	EPI	Mar-05	3 months
S B Kah	Malaya	GEN	Apr-04	10 months
F Kayat	Malaya	GEN	May-05	3 months
O Lenz	Czech	PP	Sep-04	4 months
J Lopez	Spain	PP	Oct-05	3 months
R MacSwan	UK	QHN	Jul-05	6 weeks
M Magnani	Italy	QHN	Jul-05	4 weeks
H McLellan	UK	PP	Sep-05	4 months
R Miller	UK	PP	Sep-04	9 months
M Minaeimoghadam	Iran	PP	Mar-05	6 months
I Mirowska	Poland	PP	Oct-05	6 months
Z Mulroy Hehir	Ireland	PP	Sep-05	3 months
J Neatham	UK	PP	Sep-05	8 months
A Neil	Germany	PP	Feb-05	6 months
O Okail	Ecuador	GEN	May-05	5 months
R Oliva	Ecuador	PP	Sep-05	1 month
J Oparka	UK	QHN	May-04	3 months
R Oparka	UK	QHN	Jun-04	2 months
M Opik	Estonia	EPI	Mar-04	1 month
A Pacak	Poland	PP	Nov-04	1 month
R Pack	UK	QHN	May-04	3 months
S Papineni	UK	GEN	Sep-05	4 months
R Powell	UK	QHN	Jun-04	3 months
L Robertson	UK	PP	Jul-04	3 weeks
R Rolfe	Ireland	PP	Aug-05	1 month
A Rusu	Romania	GEN	Jul-05	6 months
P Salunkhe	UK	PP	Apr-04	4 months
M Sanchez	Peru	PP	Jun-04	1 month
A M Sanz	Spain	GEN	Sep-04	3 months
S Scibetta	Italy	PP	Mar-05	6 months
R Shah	UK	PP	Apr-05	5 months
L Shang	UK	PP	Aug-05	3 months
F Shpiro	UK	QHN	Jun-04	3 months
H R Somepalli	UK	GEN	Apr-04	6 months
A Thirugnanasambandam	UK	PP	May-05	5 months
R Ulloa	Argentina	QHN	May-04	3 weeks
S Valette	France	PP	Apr-04	2 weeks
M Vicente	Portugal	PP	Feb-05	1 month
M Vitten	Germany	QHN	Sep-05	3 weeks
R Yin	China	EPI	Oct-04	2 months
D Zait	UK	GEN	Jun-05	3 months
Y Zhu	China	EPI	Mar-04	2 weeks

Longer-term visiting workers

Name	Country of origin	Programme	Month/yr of arrival	Length of stay
J Cooper	Canada	EPI	Sep-04	2 years
D Feeney	UK	EPI	Jan-04	3 years
E Lascaux	France	PP	Jun-04	3 years
S Mickowsky	UK	EPI	Jun-04	3 years
L Pylypenko	Ukraine	PP	Aug-04	1 year
T Roberts	UK	EPI	Mar-05	3 years
B Singh Bhau	India	GEN	Mar-04	1 year
R Sonnenberg	UK	EPI	May-04	3 years
I Stiller	Hungary	PP	Jul-04	1 year
M Takeshita	Japan	PP	Apr-04	1 year
A Traykova	Bulgaria	PP	Jan-05	1 year
V Turci	Italy	PP	Mar-05	1 year
S Yoshida	Japan	EPI	Mar-04	1 year
A Zakri	Germany	PP	Nov-04	1 year

Honorary Research Professors

P M A Broda MA MSc PhD DSc HonDSc
M C R Davies BSc DipTheol MPhil PhD CEng MICE FTG
G M Gadd BSc PhD CBiol DSc FIBiol
F Gunstone BSc PhD DSc FRSC FRSE CChem
B D Harrison CBE BSc PhD DAgFor FRS FRSE
N L Innes OBE BSc PhD DSc CBiol FIBiol FRSE
H G Jones MA PhD FIHort
T R Meagher BA PhD
W Powell BSc MSc PhD DSc
J A Raven PhD FRSE FRS
J I Sprent OBE BSc DSc PhD ARCS FRSE
R Viola BSc PhD

Honorary Research Fellows

F Bransby BA MA PhD
W C Christie MBE BSc PhD DSc CChem FRSE FRSC
J M Duncan BSc PhD
R P Ellis BSc PhD
A J Flavell BSc PhD
C Halpin BSc MSc HDip Ph.D
L L Handley BA BEd MSc PhD
A T Jones BSc PhD
W H Macfarlane Smith BSc PhD CBiol MIBiol FIMgt
G R Mackay MBE BSc MSc CBiol FIBiol
D K L MacKerron BSc PhD
M A Mayo BSc PhD
T Newson BSc PhD
M C M Perombelon BSc MSc PhD
D J Robinson MA PhD
A Tobin BSc MSc
D L Trudgill BSc PhD CBiol FIBiol FSON
B Williamson BSc MSc PhD DSc

Postgraduate Students

Name	Programme	Project title
J Comadran Trabel	GEN	Mapping adaptation of barley to drought environments (MABDE)
S C Conner	QHN	Metabolic profiling of potato *(Solanum tuberosum)*
S Donn	EPI	Molecular ecology of soil nematode communities
L J M Ducreux	QHN	Manipulation of carotenoid metabolism in tubers of *Solanum tuberosum* and *S. phureja* using an antisense approach
J G Morales Osorio	PP	Mechanisms of virulence and avirulence in the biotrophic interaction between potato and the late blight pathogen *Phytophthora infestans*
L Kasprowicz	PP	The population dynamics and ecophysiology of the peach-potato aphid *Myzus persicae*
J Kennedy	EPI	AM fungi in agriculture
S MacDonald	GEN	Regulatory pathways involving iron acquisition in *Pasteurella multocida* A:3, their role in pathogenesis and relevance to disease mechanisms in *Erwinia carotovora* subspecies *atroseptica*
T Miller	PP	Metabolic and proteomic profiling of the interaction between plant hosts and root knot and cyst nematode endophytes
C Mitchell	PP	Cane fruit: Novel approaches for ICM in fresh and processed crops
L Moleleki	PP	Characterization of the interaction between type three secreted proteins in *Erwinia carotovora* subsp. *atroseptica* and its host plant *Solanum tuberosum* L.
W L Morris	QHN	Characterisation and manipulation of gene expression during carotenogenesis in potato tubers
M Ravensdale	PP	Unravelling the regulatory mechanisms involved in the production of coronafacoyl phytotoxins and other pathogenicity determinants in *Erwinia carotovora* subsp. *atroseptica*
C Robert	PP	Elucidation of the regulatory binding sites in bacterial genomes
S K Sharma	GEN	Development of an efficient somatic embryogenesis system for developing synthetic seeds in potato

SCRI Research Programme

ongoing as at 1 October 2005

The research programme is commissioned by SEERAD and a variety of other funders. The list contains the body that awarded this grant and the title of the project and, in the case of SEERAD, the commissioning number is included.

SEERAD Core

SCR/540/00	Genetics of cultivated potato.
SCR/541/00	Genetic approaches to the evaluation and utilisation of soft fruit germplasm.
SCR/574/01	Development and application of metabolic profiling technologies to enhance the understanding and developmental processes in plants.
SCR/577/01	Molecular plant diversity and germplasm resources.
SCR/578/01	Parallel gene expression technologies supporting the discovery of plant and pathogen genes important to agriculture and biotechnology.
SCR/580/02	Suppression of gene silencing by virus proteins.
SCR/581/02	Cell and tissue engineering in barley and potato.
SCR/583/02	Variation in pathogenicity in *Globodera* spp. in relation to host resistance.
SCR/584/02	Approaches to regulate the L-ascorbic acid content of commercially important plants.
SCR/585/02	Genetics of cultivated diploid potatoes.
SCR/590/03	Developing physiologically based model linking genetic variation among individuals to the sustainability of biodiversity at the scale of the community.
SCR/591/03	Understanding the role and function of virus proteins in the establishment of systemic infection.
SCR/592/03	Exploitation of barley mutant populations.
SCR/593/03	Defining stability of host-pathogen dynamics of fungal leaf blights in heterogeneous barley and other graminaceous canopy structures.
SCR/594/03	Biophysical and physiological interactions at the root-soil interface.
SCR/595/03	Interpretation and application of indicators of ecosystem sustainability.
SCR/596/03	Molecular mechanisms in alternative splicing.
SCR/597/03	Population biology, molecular evolution and epidemiology of potato late blight (*Phytophthora infestans*).
SCR/598/03	An integrated and quantitative approach to the exploitation of sequence data from plant genomes.
SCR/599/03	The bioavailability and bioefficacy of soft fruit antioxidants.
SCR/600/03	Exploration and exploitation of phytochemical diversity in the Commonwealth Potato Collection through metabolite profiling.
SCR/601/03	Characterisation of novel genes from the *Erwinia carotovora* subsp. *atroseptica* genome sequence and their effects on corresponding response genes in potato.
SCR/602/03	Nuclear dynamics and small novel RNAs in the regulation of plant gene expression.
SCR/603/03	Gene based marker development for exploitation in barley.
SCR/604/03	Quantifying the role of environmental perturbation and plant genotypes in creating resilient and sustainable agroecosystems.
SCR/605/03	Interpretation of microbial functional interactions in the carbon and nitrogen cycles for the effective management of sustainable arable ecosystems.
SCR/606/03	Connecting barley genotype to phenotype with focus on grain quality traits.

SCR/607/04	Nuclear involvement in plant virus infection.
SCR/608/04	Development of durable resistance to potato and berry fruit viruses.
SCR/609/04	Floral transition of *Arabidopsis* and barley.
SCR/610/04	Produce pathogen-tested stocks of *Rubus, Ribes* and *Fragaria* and screen *Rubus* germplasm for insect resistance to support berry fruit breeding at SCRI.
SCR/611/04	Genetic basis of plant cell-to-cell communication.
SCR/612/04	Isolation of plant proteins involved in macromolecular trafficking.
SCR/613/04	Development of virus-induced gene silencing (VIGS) for high-throughput functional analysis of novel genes in plants.
SCR/614/04	Functional analyses of resistance in potato to the late blight pathogen *Phytophthora infestans* and the potato cyst nematodes *Globodera pallida* and *Globodera rostochiensis*.
SCR/615/04	Functional analysis of pathogenicity in potato cyst nematodes.
SCR/616/04	Enhancing food quality and nutritional value by exploring the limits of carotenogenesis in potato.
SCR/617/04	Construction and exploitation of a BAC library of barley cv. Golden Promise, the recently adopted 'academic reference strain'.
SCR/618/04	Integrating a physical and functional map of the red raspberry (*Rubus idaeus*) genome.
SCR/619/04	Maintenance and exploitation of genetic diversity in the Commonwealth Potato Collection and other diverse *Solanum* germplasm.
SCR/620/04	Comparative sequence analysis and the isolation of a PCN resistance QTL on potato linkage group V.
SCR/621/04	Manipulating arable plant communities to sustain a diversity resource for invertebrate trophic groups.
SCR/622/04	Manipulating crop-weed communities to optimise weed diversity and crop yield in arable systems.
SCR/623/04	An investigation of the agroecology of the peach potato aphid (*Myzus persicae*).
SCR/624/04	Development and maintenance of a database infrastructure together with analysis and visualisation tools for plant genomics data with special emphasis on gene expression, protein targeting and sequence polymorphism data types.

SEERAD Flexible Fund

SCR/833/00	Microsatellites as population genetic markers.
SCR/589/02	Novel methodologies and tools for the analysis of germplasm collections.
SCR/842/02	Elucidation of regulatory and signalling networks that control bacterial disease development.
SCR/901/02	Soil stability and resilience: the interplay between biological and physical recovery from stress.
SCR/902/02	Functional characterisation of appressorial infection stage-specific proteins from *Phytophthora infestans*.
SCR/903/02	A comparative SNP-based approach to identify and mine genes controlling root traits in the Triticeae.
SCR/906/03	Factors affecting the prevalence of clones of *Myzus persicae* in Scotland, particularly those with aphicide resistance, and implications for virus control in seed potatoes.
SCR/907/03	Viral-based functional genomics of the Golgi apparatus.
SCR/908/03	Post-genomic analysis of *Erwinia carotovora* virulence responses in *in vitro* and *in planta* environments.
SCR/909/04	Function of the exon junction complex in the plant nucleolus.
SCR/910/04	The genetics of gene expression in barley.

SCR/913/05	Characterisation and development of gene silencing in *Phytophthora infestans* for high-throughput determination of gene function.
BSS/842/04	Elucidation of regulatory and signalling networks that control bacterial disease development.
BSS/843/04	Control of pulmonary adenocarcinoma (jaagsiekte) in the Scottish sheep flock.

External research contracts

BBSRC	Stacking of novel anti-nematode and anti-feeding site factors to obtain resistance against plant parasitic nematodes.
BBSRC	UK cereal genomics consortium exploiting genomics, agri-food and environment.
BBSRC	Association genetics of UK elite barley.
BBSRC	Metabolic and proteomic profiling of interaction between plants and root knot and cyst nematodes.
BBSRC	Visualisation and modelling of plant morphogenesis: a dynamic toolkit for cell expression and fluorescent cell reporters in roots.
BBSRC	Visualisation and analysis of biological sequences, alignments and structures.
BBSRC	Targeted induced mutation discovery in barley.
BBSRC/University of Abertay	Plant root and microbial influence on soil water relations and structural stability.
British Council ARC Programme	A physically based understanding of crack genesis in soil and the impact of land management and biological processes.
British Potato Council	Developing effective integrated control measures for the control of black dot.
British Potato Council	Improving decision-making for the management of potato disease using real-time predictive diagnostics.
British Potato Council	Independent variety trials.
Commercial	Brassica breeding.
Commercial	Potato breeding.
Commercial	Molecular pathology.
Commercial	Blackcurrant breeding.
Commercial	Lipid analysis.
Defra	Prediction, sampling and management of GM impurities in fields and harvested yields of oilseed rape.
Defra	Monitoring the occurrence of GM oilseed rape volunteers in subsequent oilseed rape crops.
Defra	Factors affecting cross-pollination in maize and oilseed rape crops growing under typical UK conditions.
Defra	Molecular virology.
Defra	Crop physiology.
Defra/HGCA	GREENGRAIN: Genetic reduction of energy use and emissions of nitrogen in cereal production (LINK).
Defra/SEERAD	Molecular breeding for root-rot resistant raspberries suitable for low input growing systems (HortLINK).
EPSRC	Novel approaches to networks of interacting autonomes.
EPSRC/University of Dundee	A functional geotechnical study of how plant roots increase slope stability.

EU	ECOGEN: Soil ecological and economic evaluation of genetically modified crops.
EU	TREESNIPs: Developing single nucleotide polymorphism (SNP) markers for adaptive variation in forest trees.
EU	MABDE: Mapping adaptation of barley to drought environments.
EU	APOPHYS: Developing a physical and functional map of potato: creating new sources for molecular markers to breed cultivars with multiple resistance and quality traits.
EU	Potato late blight network for Europe.
EU	NOFORISK: Quantitative risk assessment strategies for novel foods.
EU	ALARM project.
EU	SIGMEA: Sustainable introduction of GM crops into European agriculture.
EU	SAFEFOODS: Promoting food safety through a new integrated risk analysis approach for foods.
EU	BIOEXPLOIT: Exploitation of natural plant biodiversity for the pesticide-free production of food.
EU Marie Curie	Training site in plant virology.
EU Marie Curie Fellowship	Comparative proteomics of *Arabidopsis* and human nucleoli.
EU Northern Periphery Programme	NORTHBERRY II: Domestication of northern berries.
Gatsby Charitable Foundation	Functional genomics of plant cell organelles – a novel approach using viral vectors.
HDC/SEERAD/Commercial	The breeding and commercial development of new raspberry varieties.
Royal Society	Molecular characterisation of a plant caspase.
Royal Society	Fundamental biophysical processes in the restoration of severely degraded soil by vegetation.
Royal Society	Involvement of the nucleolus in plant virus systemic infection.
Scottish Enterprise	Proof of Concept - Genetic fingerprinting for environmental monitoring.
Scottish Enterprise	Proof of Concept Plus – Vira-Tech: A platform technology for the safe biological assessment of pesticides.
Scottish Enterprise Tayside	Control of potato tuber dormancy using gibberellin biosynthesis inhibitors and the development of molecular markers for tuber dormancy.
Scottish Enterprise Tayside	New system and methods for *Agrobacterium*-mediated gene transfer: protection from plant caspase.
SEERAD Biodiversity Action Grants	The living field study centre.
SEERAD/BBSRC/GSK/HDC	Development of the physiological, agronomical and genetic tools for increasing L-ascorbic acid yield from blackcurrant bushes (HortLINK).
SEERAD/BPC/Commercial	Understanding and improving flavour characteristics of potato (LINK).
SHEFC	Scottish Bioinformatics Research Network (SBRN) maximising bioinformatics infrastructure for Scottish Health, Agriculture and Industry

Meteorological Records

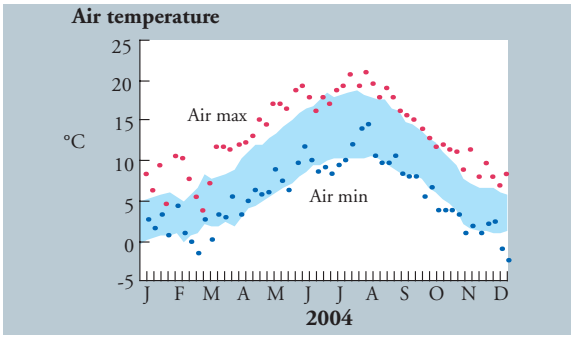
M. Grassie*

2004

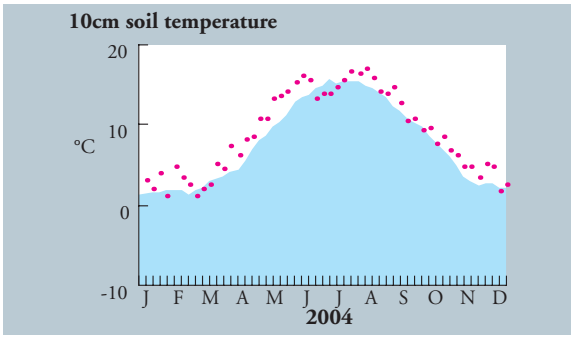
General In 2004 the SCRI meteorological station was given a much needed overhaul. A considerable amount of maintenance, instrument replacement and 'tidying up' took place. A new purpose-built shed with heat and lighting was erected as the site base, providing shelter in adverse conditions in addition to housing instruments. The larger size can accommodate much larger groups of visitors, unlike the previous model which allowed entry to only three or four at a time.

The 'met site' was visited by approximately sixteen schoolchildren in April as part of the annual Bring Your Child to Work day. During a guided exploration of the site, the children were given the chance to be involved in the day-to-day tasks required by a weather station. They made observations, read instruments and had the opportunity to ask questions.

The first of two SCRI Open days (June) also saw the site as the subject of interest for a steady stream of schoolchildren from throughout the Tayside area who, along with their teachers, enjoyed a whistle stop tour of the facility.

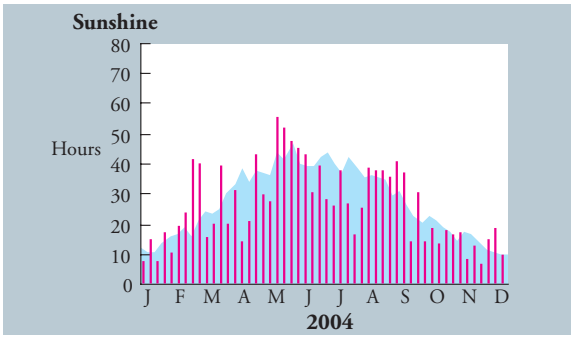


Temperature Despite temperatures generally being lower than in 2003, all average maximum temperatures were higher than typical, measured against the Long Term Average with the exception of July, slightly cooler at 18.8°C (19°C LTA). The most remarkable month was December, with an average daily maximum of 8.3°C, the highest since 1988 (6.4°C LTA).

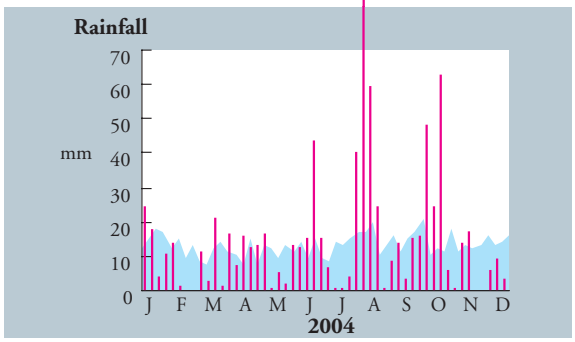


Average minimum temperatures showed a higher than normal trend throughout the summer months, in contrast to the winter months which generally displayed lower than average minimum temperatures. Only two days of frost occurred in May, against the norm of 7. All other months were close to normal.

Mean soil temperatures for 10, 20, and 30cm depths were all higher than typical; with the exception of July, which in each case was approximately 1°C lower than the LTA.

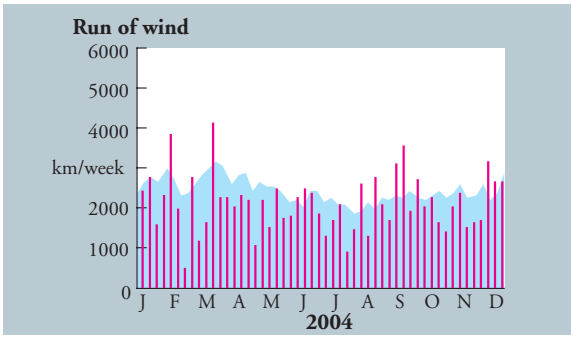


Sunshine Sunshine figures were lower than usual with a total of 1392 hours for 2004 (1411.6 LTA). April, July and August in particular fell well short of their expected quota although, in contrast, six months out of the twelve actually had higher than normal sunshine levels. February was noteworthy for receiving almost double the expected sunshine – 108.2 hours (68.2 LTA).



Rainfall The year is likely to be remembered as one of exceptional rainfall, reaching an annual total of 817.7mm compared to the LTA of 664.5. The freak weather brought flash floods and caused disastrous harvests throughout the country. Press reports claim that cereal farmers in Angus, Perthshire and Fife suffered sig-

* The long term average for 1961-1990 is shown in blue( ).
Statistics in the text are measured against the monthly Long Term Average (LTA) for 1971 to 2000.



nificant losses during the worst month, August, which proved to be the wettest since SCRI records began in 1954. Perhaps surprisingly, eight out of the twelve months showed lower than average rainfall. February was a particularly dry month with only 15.8mm rain set against the LTA of 47.1. The deluge was restricted to four months: April, which had 59.4mm (44.6 LTA); June, with had 94.2 (51.7 LTA); October, with 155mm (67 LTA); and in particular, August with 256.3mm (52.3 LTA).

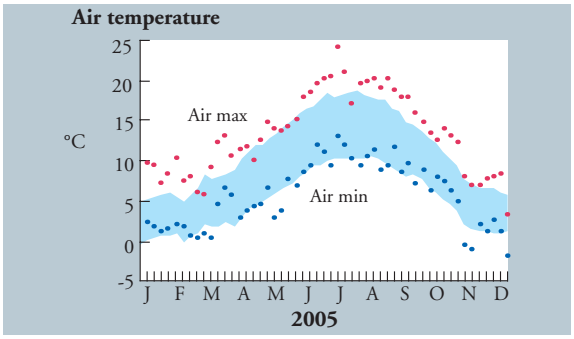
Wind Overall, windspeeds were unexceptional. The highest being the months March, October and November, which all had at least 1 day with speed of 20+ knots reached (representing a 'fresh breeze' on the Beaufort scale), and February and December which had 1 day at 25 and 24 knots, respectively ('strong breeze').

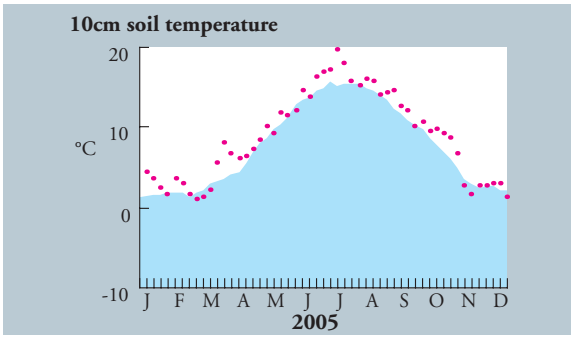
The Unusual Local press reported several sightings of a 'tornado like' phenomenon to the north of Dundee in late April.

2005

General Once again, in April the SCRI met station was the attraction for approximately nine schoolchildren involved in the annual Bring Your Child to Work day. The children spent the morning participating in 'glasshouse activities' which included the informative visit to the site, where they learned about (and tried out) observing and recording our weather with one of SCRI's trained observers. Sadly, the weather was not in our favour, it being a morning of heavy rainfall. However, the new larger Met shed proved invaluable as shelter from the worst of the elements.

Temperature Conditions were generally warmer, with all months showing average maximum temperatures higher than the Long Term Average, without exception. The most remarkable being January, the highest since 1989, at 8.9°C (LTA 5.9°C), with ten individual days achieving between 10°C and 13°C; and September, with an average of 18°C being the second warmest since 1959 (also 18°C, beaten only by 18.3°C in 1999). Although 2003 will be remembered for its hot summer, 2005 actually exceeded some of its maximum temperatures, with an individual day in July reaching 28.2°C.

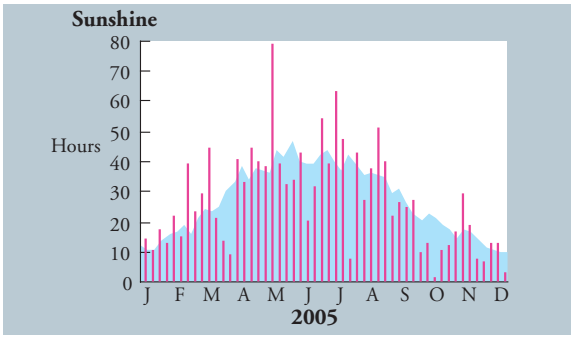




This year was also remarkable in the length of the warm spell. This extended as far back as March (16.2°C on the 25th), and 18.1°C on the 1st April and into autumn with 23°C on the 6th September, and 17.9°C on the 27th October.

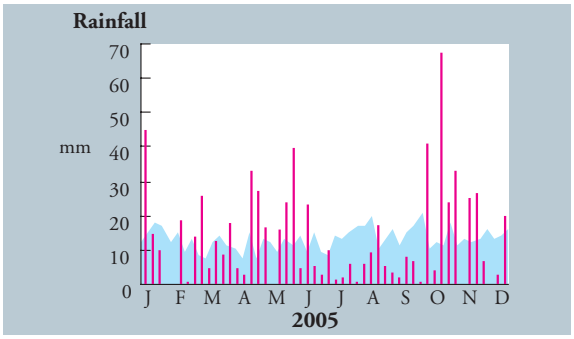
Similarly, average minimum temperatures were higher than typical with the exception of May, August, and November, which were all slightly lower than the LTA. March displayed the highest average minimum since 1990, at 3.7°C (2.0°C LTA). Only one day's frost occurred in October, against the norm of 9.5; January and March also having less than normal with 18 and 13 days respectively (23.5 and 17.5 days LTA). Contrarily, May had 13 occurrences compared to the LTA of 7.

Mean soil temperatures were generally higher than the LTA with the exception of February, May and November (fractionally cooler at 10cm depth); November and December (slightly cooler at 20cm). At 30cm depth all but one (which was equal to) was higher than the LTA.

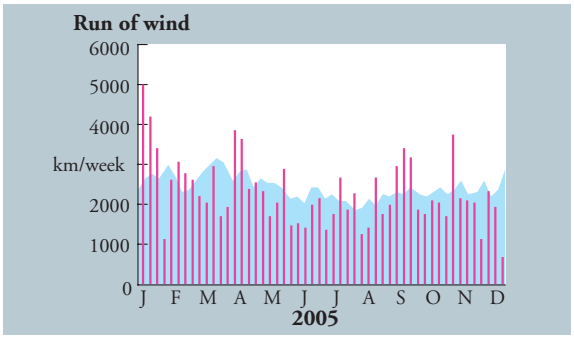


Sunshine and Solar Radiation Sunshine figures were very close to normal with a total of 1419.4 hours (1411.6 LTA), with six months showing higher than average figures and six showing lower. Only two months were worthy of note: February, with sunshine amounting to 94.5 hours, compared to only 68.2 LTA; and October, which received only 48.5 hours sunshine, half of the expected 94.5

Solar radiation values were unexceptional, except for October which, unsurprisingly, was lower than normal.



Rainfall Generally, rainfall was higher than normal, the annual total reaching 714.2mm as compared to the LTA of 664.5mm. Particularly wet were October and November, which received 119.7 and 80.2mm rain respectively (67 and 52.1 LTA). October brought flood conditions after the heavy rainfall on the 24th (36.8mm). Although January rainfall was not greatly higher than normal (76.1mm, compared to LTA of 67.9), it all fell within the first eighteen days of the month, 28.9mm falling on the 7th alone. Coupled with the month's high winds, this resulted in storms causing widespread flooding, particularly in Perthshire. The main exception to this was the period from July to September when a total of only 77.4mm fell. Expected rainfall for this period is 169.4mm.



Wind For most of the year, wind speeds were unexceptional. March and April had at least one day with a mean speed of 20 knots reached at the time of recording (representing a 'fresh breeze' on the Beaufort scale), while January and August had days which reached over 24 knots ('strong breeze'). January in particular will be remembered for its severe gales which caused extensive damage in Dundee and throughout Scotland, involving damaged roofing and uprooted trees. SCRI recorded four days of gales (mean wind speeds reaching 34 knots) between the 6th and 12th, with gusts reaching 56 knots.

Institutes supported by the Biotechnology and Biological Sciences Research Council

BBSRC Office	Polaris House, North Star Avenue, Swindon, Wilts SN2 1UH	01793-413200
BBSRC Bioscience IT Services	West Common, Harpenden, Herts AL5 2JE	01582-714900
Babraham Institute	Babraham Research Campus, Cambridge CB2 4AT	01223-496000
Institute for Animal Health		
Compton Laboratory	Compton, Newbury, Berkshire RG20 7NN	01635-578411
Pirbright Laboratory	Ash Road, Pirbright, Surrey GU24 0NF	01483-232441
BBSRC & MRC Neuropathogenesis Unit	Ogston Building, West Mains Road, Edinburgh EH9 3JF	0131-667-5204
Rothamsted Research		
Rothamsted	Harpenden, Herts AL5 2JQ	01582-763133
Broom's Barn	Highham, Bury St. Edmunds, Suffolk IP28 6NP	01284-812200
Institute of Food Research	Norwich Research Park, Colney, Norwich NR4 7UA	01603-255000
Institute of Grassland and Environmental Research		
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North Wyke Research Station	Okehampton, Devon EX20 2SB	01837-883500
Bronydd Mawr Research Station	Trecastle, Brecon, Powys LD3 8RD	01874-636480
Trawsgoed Research Farm	Trawsgoed, Aberystwyth, Dyfed SY23 4LL	01974-261615
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Scottish Agricultural and Biological Research Institutes

Hannah Research Institute (Until March 2006)	Ayr, Scotland KA6 5HL	01292-674000
The Macaulay Institute	Craigiebuckler, Aberdeen AB9 2QH	01224-498200
Moredun Research Institute	Pentlands Science Park, Bush Loan, Penicuik, Midlothian EH26 0PZ	0131-445-5111
Rowett Research Institute	Greenburn Road, Bucksburn, Aberdeen AB21 9SB	01224-712751
Scottish Crop Research Institute	Invergowrie, Dundee DD2 5DA	01382-562731
Biomathematics and Statistics Scotland (Administered by SCRI)	University of Edinburgh, James Clerk Maxwell Building, King's Buildings, Mayfield Road, Edinburgh EH9 3JZ	0131-650-4900

List of Abbreviations

AAB	Association of Applied Biologists
ACRE	Advisory Committee on Releases to the Environment
ADAS	Agricultural Development and Advisory Service
ATCC	American Tissue Culture Collection
BBSRC	Biotechnology & Biological Sciences Research Council
BCPC	British Crop Protection Council
BioSS	Biomathematics and Statistics Scotland
BPC	British Potato Council
BSPB	British Society of Plant Breeders
BSPP	British Society for Plant Pathology
BTG	British Technology Group
CAPS	Cleaved Amplified Polymorphic Sequence
CEC	Commission of the European Communities
CEL	Crop Evaluation Ltd
CHABOS	Committee of Heads of Agricultural and Biological Organisations in Scotland
CIP	International Potato Centre - Peru
COST	European Co-operation in the field of Scientific and Technical Research
CRAFT	Co-operative Research Action for Technology
Defra	Department for Environment, Food and Rural Affairs
DfID	Department for International Development
EAPR	European Association for Potato Research
ECOGEN	Soil ecological and economic evaluation of genetically modified crops
ECRR	Edinburgh Centre for Rural Research
ECSA	European Chips and Snacks Association
EHF	Experimental Husbandry Farm
ELISA	Enzyme linked immunosorbent assay
EPICA	European Project for Ice Coring in Antarctica
EPPO	European Plant Protection Organisation
EPSRC	Engineering and Physical Sciences Research Council
ER	Endoplasmic Reticulum
ESTs	Expressed Sequence Tagged Sites
EUCARPIA	European Association for Plant Breeding Research
FF	Flexible Funding (SEERAD)
FLAIR	Food-Linked Agro-Industrial Research
FSA	Food Standards Agency
FSE	Farm Scale Evaluation
GC-MS	Gas Chromatograph-Mass Spectrometer
GFP	Green Fluorescent Protein
GILB	Global Initiative on Late Blight
GIUS	Glasshouse Investigational Unit for Scotland
GM	Genetically Modified
GMHT	Genetically Modified Herbicide Tolerant
HDC	Horticultural Development Council
H-GCA	Home-Grown Cereals Authority
HPLC	High Performance Liquid Chromatography
HRI	Hannah Research Institute
HRI	Horticultural Research International
ICARDA	International Center for Agricultural Research in Dry Areas
ICTV	International Committee for the Taxonomy of Viruses
IIP	Investors in People
IITA	International Institute of Tropical Agriculture
IMP	Individual Merit Promotion
IOBC	International Organisation for Biological Control
ISHS	International Society for Horticultural Science
ISPP	International Society for Plant Pathology
ITMI	International Triticeae Mapping Initiative
IVEM	Institute of Virology and Environmental Microbiology
LC-MS	Liquid Chromatograph-Mass Spectrometer
LEAF	Linking Environment and Farming
MLURI	Macaulay Land Use Research Institute (now the Macaulay Institute)
MRI	Moredun Research Institute
mRNA	messenger RNA
MRS	Mylnefield Research Services
NERC	National Environmental Research Council
NFT	National Fruit Trials
NFU	National Farmers Union
NIR	Near Infra-Red
NMR	Nuclear Magnetic Resonance
NPTC	National Proficiency Test Council
ORSTOM	Organisation for research in science and technology overseas
PCN	Potato Cyst Nematode
PCR	Polymerase Chain Reaction
PD	Post-doctorate
PIC	Product Innovation Centre
PVRO	Plant Variety Rights Office
RACER	Reduced Application of Chemicals in European Raspberry Production
RAPD	Randomly Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism
RNAi	RNA interference
RRI	Rowett Research Institute
RSPB	Royal Society for the Protection of Birds
SABRI	Scottish Agricultural and Biological Research Institutes
SAC	Scottish Agricultural College
SASA	Scottish Agricultural Science Agency
SCRI	Scottish Crop Research Institute
SEB	Society for Experimental Biology
SEERAD	Scottish Executive Environment and Rural Affairs Department
SET	Scottish Enterprise Tayside
SNH	Scottish Natural Heritage
SNSA	Scottish Nuclear Stocks Association
SPD	Senior Post-doctorate
SSCR	Scottish Society for Crop Research
STS	Sequence Tagged Sites
UNDP	United Nations Development Programme
USA NSF	USA National Science Foundation
VIB	Flemish Institute of Biotechnology
WHO	World Health Organisation