Genetics

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In Genetics we conduct fundamental, hypothesis-led research supported by the development of biological resources and enabling technologies that underpin applied genetics research and product delivery. Over the last year we have begun the process of re-focussing our research programmes on some of the challenges raised by climate change, environmental concerns and the demand for healthy and nutritious food and feed. Thus we have realigned our research to encompass priorities that include tolerance to abiotic stress and lower input agriculture.

We fundamentally believe that a strong portfolio of basic research is necessary to fuel discovery and to develop the understanding required for innovation and future applications. However, a major aim is also to translate our research outcomes into approaches and technologies that enable genetic research in crops – particularly barley, potatoes and soft fruits – that underpin the Scottish agricultural sector. To enhance this process, we participate in national and international initiatives with academic and commercial partners to maintain the profile of our research and ensure its direct relevance to practical outcomes. We continue with active crop improvement programmes, working with industry to deliver products to the marketplace. Currently, Genetics contains approaching ninety staff, including three fully integrated research active groups from the University of Dundee (C. Halpin, A.J. Flavell and G.C. Simpson). A separate report from these groups follows. This brief overview contains research highlights from Genetics in 2006 that are not represented in the following, more detailed, scientific reports.

Over the last year we have extended our characterisation of the plant nucleolus, a major sub-nuclear organelle. The nucleolus is involved in a wide range of gene expression processes, but more recently it has been shown to act as a sensor of cellular stress in animal cells and to be involved in aspects of gene silencing in plants. With Peter Shaw at John Innes Centre (JIC), using a combined proteomics and RNomics approach, we have demonstrated a role for the nucleolus in mRNA export and degradation. In an entirely novel finding, we have demonstrated that some naturally-occurring antisense transcripts (NATs) are enriched in the nucleolus. NATs are likely to be involved in specific gene silencing and one of these has been shown to regulate gene expression in response to salt stress through the RNA interference pathway. The precise role the nucleolus plays in these processes remains a key question. More widely, many processes contribute to the overall regulation of gene expression during development and environmental challenge. Investigations into the role of alternative splicing are described by Craig Simpson and others in a following article.

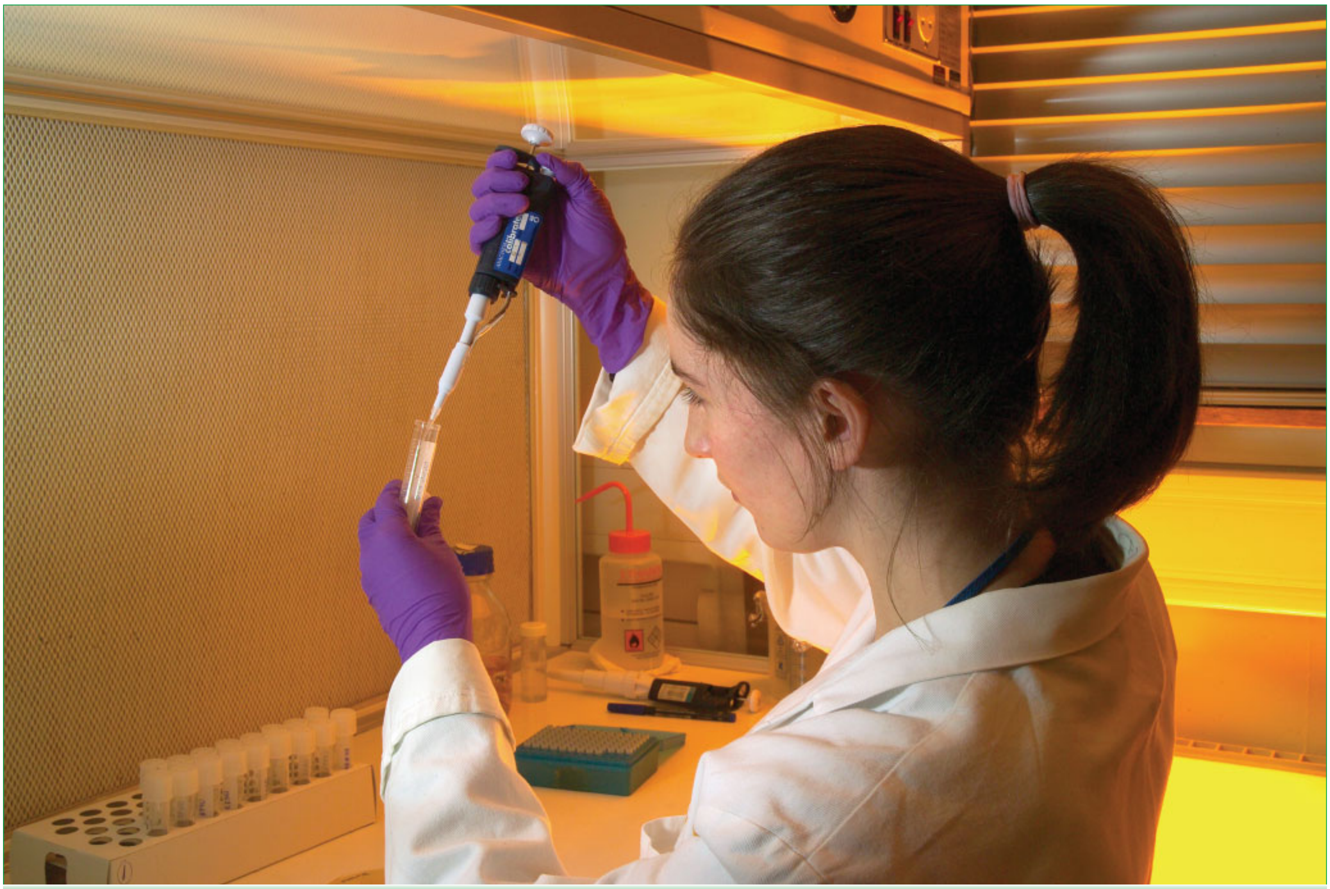
By exploring the genetic control of mRNA abundance in different plant genotypes we have been linking RNA-biology with genetics. We measured the abundance of more than 21,000 different barley mRNA species along with approximately 20 phenotypic traits in a segregating doubled haploid population. With Mike Kearsey in Birmingham University, we conducted linkage analysis, treating individual mRNA abundances as quantitative traits (QT) and identified thousands of genes showing highly heritable mRNA abundance levels. Hundreds of these are highly associated with phenotypic trait locations and a subset, strong regulatory and/or positional candidate genes, are under detailed investigation.

In all our studies, we consider it crucial that we correlate molecular data with classical phenotypic traits. In a collaboration with NIAB, analysis of multiple small barley mapping populations has highlighted the dependence of characters such as fermentability upon wort sugars (principally maltose) and revealed the close relationships between the activity levels of enzymes in the malting process that are regulated by the plant hormone gibberellic acid. With Jose-Luis Molino-Cano in Lleida, Spain, we identified three QT loci for grain β-glucan content. This is directly relevant to malting quality as low levels of β-glucan, a major component of barley endosperm cell walls, are important in the brewing and distilling industries. The largest QT locus co-locates with the hulless (naked) gene. As hulless barley is generally high in β-glucan, a compound with proven cholesterol-reducing effects, this linkage could be exploited through breeding to generate barleys tailored for human nutrition. In future, many more such linkages will be identified in a UK-wide collaboration using the approach described by Luke Ramsay and others in a following article.

Our studies in barley are possible because of its well developed genetics. However, last year, we also produced the first genetic linkage map of blackcurrant (*Ribes nigrum* L.) and screened many important phenological, agronomic and fruit quality traits in the mapping population. This is described further in the article by Rex Brennan and others which follows. In raspberry, we have previously shown that Gene H is associated with resistance to cane botrytis and spur blight, but not with cane spot and yellow rust. Markers have been identified linked to the four diseases. Gene H has been mapped and is now the focus of a positional cloning effort. Importantly, in July this year we released a new raspberry cultivar, Glen Doll, our first in 10 years.

Exploiting biodiversity has underpinned the development of new SCRI cultivars. Last year we extended our molecular analysis of the Commonwealth Potato Collection (CPC) to describe diversity in wild and cultivated species from different geographic origins, ploidy and breeding systems. We confirmed that there is considerably less genetic diversity among accessions of self-compatible as compared to self-incompatible taxa. However, diversity among individuals drawn from different accessions was of similar magnitude in self-compatible and self-incompatible species, with the former showing only slightly lower rates of polymorphism. The most diverse accessions were the cultivated potato accessions, and the least, the Mexican polyploids. Thus, for diversity and phylogenetic studies, a single plant is highly representative of inbreeding or moderately outbreeding accessions while for highly heterozygous self-incompatible species, a deeper sampling of more individuals is advisable. These observations have significant implications for the *ex situ* maintenance of *Solanum* germplasm in genebanks such as the Commonwealth Potato Collection (CPC) held at SCRI.

Testament to the potential benefits of exploiting biodiversity, the launch of the new SCRI-bred cultivar Mayan Gold (*Solanum tuberosum* Group Phureja, also known as *S. phureja*) by Greenvale AP, made the UK National



News. It is the first potato from this group to be commercialised outside of South America and is derived from the diploid cultivated potatoes of Venezuela, Colombia, Ecuador, Peru and Bolivia. It has an interesting flavour and makes excellent French fries and roast potatoes. Greenvale AP have also successfully established Vales Emerald as an early punnet type and Vales Sovereign for prepack. Lady Balfour now commands approximately 40% of organic maincrop production. It has field resistance to late blight derived from the Mexican wild species *S. demissum* and partial resistance to cyst nematodes derived from the South American wild species *S. vernei.* Vales Everest has the best resistance to the white potato cyst nematode, *Globodera pallida*, of any cultivar on the UK National List. Its resistance is derived from an Andigena potato accession in the CPC.

Genetics manages two Institute-wide research facilities. First, the Sequencing Service provides a complete 'DNA template to data' pipeline in a highly efficient and cost-effective manner that is widely used by all Programmes across the Institute. Second, the Microarray facility completed numerous collaborative projects including key publications on an analysis of dormancy control in *Rubus* and pathogenicity studies in *Erwinia*.

Finally the changes in Institute status have reinforced the need for each Programme to win competitive research funding from a diverse range of sponsors. Last year we secured major new funding from the Crop Science Initiative, ERA-PG, Generation Challenge programme, EU-Sol, IAEA and EU-FP6. These successes are firmly based in the quality and competitiveness of our science. They will enhance our research and development portfolio and help us remain agile in an increasingly competitive research environment.