Genetics

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

Several barley projects have focused on using a high throughput molecular marker platform based on *Illumina*'s Oligo Pool Assay (OPA). Bill Thomas, Luke Ramsay, Joanne Russell and Andy Flavell (Division of Plant Sciences – DoPS) have assembled extensive collections of barley germplasm that include cultivars, globally distributed landraces and wild collections. As well as characterizing the extent and distribution of genetic diversity in these collections, they have been exploring whether the approach termed 'association mapping' can be successfully applied to locate the genes controlling a range of phenotypes (see article by Joanne Russell and colleagues). The genetic information revealed by the OPA, combined with historical and newly assembled phenotypic data, has enabled them to identify regions of the genome that have been selected during genetic improvement of both monogenic and polygenic traits including yield and malting quality. For example, in European spring barley they have recently identified allelic changes at multiple loci selected for during the breeding progression from the highly successful landmark cv. Triumph to the cv. Westminster (first recommended in the UK in 1980 and 2005 respectively), covering an improvement of over 3% in hot water extract. Given these successes we intend to develop OPA's for both potatoes and soft fruits.

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

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

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

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

Last year we significantly expanded our research on 'extreme phenotypes' of barley. Frequently the result of chemically or physically induced mutations, they comprise a new focus for the barley program which is also enhancing interactions with DoPS (and other universities). Individual mutants altered in inflorescence development, leaf and root morphology and the fundamental process of recombination have been entered into an intensive crossing programme to develop segregating populations required for positional cloning. Investigating fundamental aspects of grain development, genes responsible for grain shape are being sought by David Leader and Arnis Druka. In collaboration with Claire Halpin (DoPS), mutants have been identified that have altered lignin content, and these are being investigated for their potential as increased digestibility feedstocks and for bio-energy production. As they potentially impact plant development, yield and quality, inflorescence mutants are being investigated in collaboration with Dr. Gordon Simpson (DoPS).

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

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

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

in RNA processing may mediate responses to different ambient temperatures.

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

With such complex and large datasets (last year we collected over 12M genotypic datapoints for barley alone) we rely increasingly on appropriate bioinformatics and statistical tools to store, analyse and display our results. The GERMINATE database and associated tools developed by the Bioinformatics group led by David Marshall (and Andy Flavell (DoPS)) has been adapted and optimised to handle genotype data from the OPA platform. GERMINATE can handle data sets with an excess of 30,000 plot records for a single trait. Current developments include a graphical interface that enables users to visualise data summaries directly from database queries. Of particular practical importance has been the visualisation of genotype data either directly from the database through the web interface or on larger scale using the Java-based Genotype Visualisation Tool (GVT) that enables users to compare, sort or cluster high resolution graphical genotypes from a large number of plant lines.

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

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