Genes to Products

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Within the UK there are clear indications that the transfer of knowledge from model plant systems to crop plants will be a key driver for research funding and product development in the public sector. The SCRI and the Genes to Products Theme are already well positioned to deliver next generation crop plants that fulfill a range of end-user requirements. Multidisciplinary approaches and key strategic alliances (academic and commercial) will be continually fostered to maintain our uniqueness and relevance.

Quality, Health & Nutrition Programme The driving force for the programme is to understand the processes which regulate specific quality and nutritional parameters of our important commodity crops. This combines the skills of natural product chemists, biochemists, molecular biologists and the genetic/breeding skills of the sister programme, Genome Dynamics. Important linkages include those with the University of Dundee Medical School with whom a joint initiative on the nutritional qualities of plant based foods has been established. Metabolite profiling continues to provide an increasingly important technology platform used within the programme, recently assisted by significant grant income from EU Framework VI. Particular attention is focused on the potential to detect unintended effects in GM crops but with a growing remit to understand compositional variability associated with low and high input crop management systems. Thus far metabolite profiling, using potato as a model system, has shown that natural variation (comparisons of varieties and landraces) in the metabolites measured outweighs any differences between GM lines and their appropriate controls. However, it was possible to distinguish specific GM lines from their parents. In addition, there were clear examples of metabolite changes induced in tubers derived from plants generated through tissue culture (non-GM) suggesting that somaclonal variation may represent an important source of unintended effects. Metabolite profiling is also being used to assess associations between raw and processed food quality. For example, increased levels of branched amino acids and methionine in raw potato has been correlated with the production of methional and branched aldehydes, alcohols and esters, reported as key contributors to the characteristic aroma of cooked potato.

Transgenic potato plants have been generated in which the tuber carotenoid content has been enhanced up to 7-fold. Non-transgenic potato germplasm contains negligible amounts of the provitamin A carotenoid, β-carotene, whereas some of the transgenic lines developed contain nutritionally significant levels of β-carotene. Detailed analysis of the potato transgenics (including the use of microarrays and metabolite profiling), is in progress with the aim of understanding how carotenogenesis is regulated. The function of candidate regulatory genes is being assessed using virus-induced gene silencing (VIGs) whilst a protocol for stable transformation has been developed for the normally recalcitrant, high carotenoid-containing diploid species, *S. phureja*. Whilst total carotenoid levels are naturally high within accessions of this species, transgenic approaches have again been successful in increasing the total carotenoid level in tubers by 3- to 4-fold. Collaborations with the Genome Dynamics Programme aim to use association genetics to identify alleles that give rise to high tuber carotenoid levels.

Further progress has been made in understanding how the availability of nutritionally important phytochemicals may be modified in humans. This exploits an *in vitro* digestion model which has shown that the digestion of putatively beneficial soft fruit phenolics is dependent on both ring hydroxylation and glycosylation. Using raspberry fruit, the constituent anthocyanins and ellagitannins were shown to be hydrolysed to small pharmacologically active molecules. Other studies have revealed that specific anthocyanins and ellagitannins inhibit the mammalian starch digestive enzymes α-glucosidase and α-amylase, respectively. This could have direct implications on the availability of simple soluble carbohydrates in the diet.

Genome Dynamics Strategically, biological links between functional, gene-based markers and target phenotypes are being highlighted. For example, genome-wide transcription profiling studies have been used to assemble a collection of ~2,500 barley genes which are responsive to important abiotic stresses by switching on or off. Approximately 1,500 of these genes have been re-sequenced in a number of cultivars revealing differences (single nucleotide polymorphisms or SNPs) which are being used to map them on to the barley genome. In a similar way we are investigating malting quality and yield (see following article by Macaulay *et al.*) and have identified genetic markers associated with hot water extract and epi-heterodendrin production. These markers have potential intellectual property value and will be added to the suite of other markers developed and commercialised by the barley genetics programme.

With regard to barley disease resistance, re-sequencing of the *Mlo* locus (plants carrying loss of function alleles are resistant to all known isolates of powdery mildew) has indicated that the *mlo*-11 allele likely arose just once after barley domestication. Collaboration with the groups of Prof. Paul Shulze-Lefert and Ralph Panstruga (Max Planck Institute, Köln) has shown that resistance is linked to a complex tandem repeat array consisting of 3.5 kb regulatory and 1.1 kb coding sequence inserted upstream of the wild-type gene. It is likely that this array acts as a transcription factor sink leading to *cis*-dependent perturbation of transcription machinery assembly by transcriptional interference. This specific example clearly demonstrates how changes in transcription of a single gene can have a major effect on plant phenotype. A global analysis of genotype-dependent gene expression is described in the following article by Druka *et al.*

Last year we reported that the Commonwealth Potato Collection had been genetically fingerprinted using molecular markers. This year, analysis of the resulting data is providing significant insight into the evolution of the cultivated potato and guiding exploitation through other research programmes at SCRI (see following article by Bryan *et al.*). For example, novel resistance against potato cyst nematode (PCN) and late blight has been identified and is already in the early stages of introgression into the cultivated genepool. Based on the application of molecular markers, the theory of linkage and quantitative trait locus (QTL) analysis, developed at SCRI in collaboration with BioSS, has been successfully applied to the analysis of quantitative resistance to late blight, which remains a potentially devastating disease. This work represents an effective collaboration between geneticists, pathologists and statisticians at SCRI. Along similar lines, a marker linked to the hypersensitive reaction to *Tobacco Rattle Virus* (TRV) the cause of spraing symptoms in the flesh of potato tubers has been identified. A further major gene conferring true resistance to TRV has also been identified.

The new early maincrop potato cultivar Vales Sovereign (superior cooking qualities, good resistance to several important diseases, suitable for Integrated Crop Management production) was added to the National List in 2003 (marketed by Greenvale AP). In addition, a new *Solanum phureja* potato cultivar, Inca Dawn, was also added to the National List in 2003. It is a novelty salad type, with deep yellow flesh colour due to a high carotenoid content and illustrates a clear scientific linkage with the Quality, Health & Nutrition Programme.

Construction of a genetic linkage map of a target species is considered the entry point into detailed genetical studies and facilitates the identification of markers that can be subsequently used to predict and follow traits in the progeny of crosses between chosen parental lines. The article by Graham *et al.* describes the development and use of the first genetic linkage map of red raspberry. In addition, a publicly available red raspberry BAC library (cultivar Glen Moy) has been developed comprising over 15,000 clones with an average insert size of approximately 130 kb and less than 1% contamination with chloroplast and mitochondrial DNA, respectively. In combination with the mapping studies this library represents the platform for map-based gene isolation in *Rubus*. Linkage mapping in blackcurrants has progressed more slowly, largely due to a lack of polymorphism between the parental lines of the mapping populations and issues with many of the markers that appear to reside in repetitive DNA. Nevertheless, the application of modern breeding technologies remains successful and productive. Blackcurrant cultivars ‘Ben Hope’ and ‘Ben Gairn’, the first commercial processing cultivars with resistance to gall mite and reversion virus, respectively, are currently enjoying considerable commercial success throughout Europe, and new seedlings with further improvements in agronomic and quality characters are in final farm-based trials.

Finally, we continue to have significant input into issues related to biodiversity and the erosion of genetic diversity. In collaboration with the Royal Botanic Garden Edinburgh, considerable progress has been made in understanding natural populations of *Koenigia islandica* and *Anastrophyllum joergensenii* and related species through the discovery of molecular polymorphisms. Our observations have led to further work examining a Scottish liverwort population (thought to be *A. joergensenii*) which appears to be a new taxon.