Genes to Products

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'Genes to Products' aims to harness the combined power of genomics, contemporary genetics, biochemistry and natural product chemistry to deliver products to market places becoming increasingly sophisticated and competitive. Breeding is seen as a crucial platform for product development but the delivery of high quality, relevant science, is also key to the vision as is the continued development of truly interdisciplinary approaches in problem solving activities. Activities in this Theme will be closely integrated with the development of newly established Product Innovation Centres (PIC) for SCRI's major commodity crops: potato, fruit and grains, each driven by a lead scientist. The PIC falls under the umbrella of Mylnefield Research Services (MRS).

The Genes to Products Theme has two research programmes, Quality, Health & Nutrition (QHN) and Genome Dynamics (GD).

Quality, Health & Nutrition: The goal of the QHN Programme is to implement strategies to improve the quality and nutritional value of raw materials entering the food chain. Traditionally, crops have been bred for high yield and disease resistance. The programme focuses on phytochemicals, which have potentially important roles in human health and on the identification of compounds and processes, which contribute to the flavour and textural properties of food materials. Metabolite profiling has been developed as an underpinning platform technology and is being deployed to assess phytochemical diversity and to unravel the metabolic networks that regulate the development of key traits. The utility of the technology in the detection of unintended effects in GM crops is also being addressed within the framework of national and European consortia.

Research on antioxidants and bioactive molecules focuses on phenolic antioxidants, L-ascorbic acid and carotenoids using a range of phytochemical, biochemical and molecular approaches. *In vitro* digestion studies have shown that fruit anthocyanins are subject to non-specific absorption e.g. on to bile acids and undergo chemical hydrolysis during digestion (and prior to absorption). Significantly, chemical transformations of phenols to ortho-phenolic acids (aspirin analogues) have been detected with substantial biological implications for human health given that aspirin is the leading drug recommended to retard the development of cardiovascular disease. Research on L-ascorbic acid has focused on the plant biosynthetic pathway and turnover in storage organs. In addition, long-distance transport of L-ascorbic acid in crop plants has been demonstrated and novel approaches for the cloning of plant L-ascorbic acid transporters developed. Carotenogenesis in potato has been characterised in detail, focusing on transcriptional changes in genes that encode the major carotenoid biosynthet-

ic enzymes (use of germplasm with high xanthophyll content). Gene targets for the manipulation of tuber carotenoid content have been already identified and functional studies are underway using stable transgenic approaches and, in collaboration with the Cell-to-Cell Communication Programme, viral-induced gene silencing.

Research on organoleptic properties of potato tubers has identified some eighty volatiles produced by cooked samples. Significant quantitative differences in headspace components have been found in germplasm adapted by breeders in the GD Programme, germplasm known to have distinct organoleptic properties. These findings are being exploited to identify the genes involved in flavour generation (cloning, mapping).

Substantial progress has been obtained in protocol development for metabolic profiling using potato tubers as the primary model system for the development of the technologies and assembly of mass spectral databases (GC-MS and LC-MS). Currently *c.* 900 compounds can be separated by combined LC- and GC-MS approaches. The technology is being applied to food safety issues (unintended effects in GM crops) and to determine phytochemical diversity in germplasm collections.

Genome Dynamics: A major objective of the GD Programme is to identify genes (or closely linked markers) controlling important traits in our mandate crops and to use these in the development of improved germplasm. Over the last year significant progress has been made in integrating genomics and informatics technologies and resources with more traditional skills in genetics and plant breeding. The primary molecular tools and competencies exploited are based on the efficient detection and analyses of molecular polymorphism. Throughout the programme, genetic mapping and analyses of the spectrum, frequency and distribution of genetic diversity are being investigated at levels ranging from individual candidate genes, through chromosomal regions to the entire genome. These primary tools have been supplemented by an expanding array of 'genomics' resources such as BAC libraries, microarrays and reverse genetics populations which present new opportunities for understanding the structure and organisation of the plant genome and the transcriptome, and provide a route towards gene isolation and function testing. The tasks of assembling appropriate genetic populations and assaying them for a wide range of important phenotypes are viewed as crucial to our ability to exploit these tools.

The potato research programme is firmly based on the exploitation of the extensive genetic diversity present within the Commonwealth Potato Collection. Last year its conversion into a curated DNA bank with base and working collections of both single plant and accession bulks of DNA was completed. In addition the entire collection (*c.* 1400 accessions and ~600 accessions from the Sturgeon Bay collection in the USA) has been genetically fingerprinted with molecular markers (see following article by McLean, Bryan, Ramsay and colleagues). Importantly, the molecular and phenotypic characterisation of the CPC is guiding its exploitation e.g. in identifying novel, broad spectrum resistance to PCN and novel quality traits. Detailed QTL maps of the two most important sources of resistance to the PCN species *G. pallida* have been developed. Last, but not least, a novel strategy for potato breeding has been published as a culmination of 12 years of research. The strategy is now being introduced into our commercially funded potato breeding programmes.

In the soft fruit research programme, considerable progress has been made in the assembly of enabling technologies for genetics and breeding (informative SSR markers for Rubus and Ribes) and these have been used to construct the first genetic linkage map of the red raspberry *R. idaeus.* Ribes populations have also been developed which focus on fruit quality characteristics which complements the objectives of QHN, our sister programme. These populations have been established as 'living' mapping resources that will be invaluable for conducting the extensive phenotypic analysis required to link genes to phenotypes. The soft fruit programme has had continued success in developing commercial cultivars with new Rubus seedlings combining root rot resistance with fresh market quality and Ribes seedlings with both pest resistance and high ascorbate content progressing rapidly along the route to commercial production.

As a general approach towards the identification of genes controlling traits of interest in barley, considerable progress has been made in assessing the applicability of association genetic studies by developing an understanding of linkage disequilibrium (LD) and some of the factors, which influence it. For example, a detailed investigation across the hardness locus (*Ha*) at the distal end of 5HS has given considerable insight into LD in barley at the ultimate resolution – DNA

sequence. These resulting observations are important because they show that such studies are feasible in barley. As a result, LD will be a key approach to candidate gene identification and validation via haplotype analysis. QTL mapping in barley based on composite populations from small progenies from a number of elite crosses has also been initiated. An ongoing objective is the development of SNP and EST-SSR based molecular markers to streamline molecular mapping via population based studies and association genetics.

Two significant contributions have been made towards realising functional genomics studies in barley. Firstly, collaboration with the global barley genomics community has been implemented to exploit the EST collections developed at the SCRI and elsewhere to commission the fabrication of an AFFYMETRIX GeneChip microarray (23,000 unique barley genes). Secondly, to facilitate functional studies on a genomic scale, large, structured mutant EMS and sodium azide populations of cv. Optic and cv. Golden Promise, respectively, have been constructed, evaluated and used for the first time to identify mutations in target barley genes by reverse genetics. There is great potential for using mutants to understand developmental or biochemical processes. Therefore, in addition to the mutant populations, we have developed a series of populations segregating for major morphological mutations as a resource for future gene isolation projects.