

Genetics

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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 resist-

ance 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.*