Grass Traits and Varieties

Mike Humphreys

New developments and technologies  13
Technologies for trait analysis  15
Conclusions  15
The Grass Traits and Varieties (GTV) programme represents research on a wide breadth of target traits relevant to new objectives aimed at designing improved forage or amenity grass cultivars that will be capable of providing UK grasslands with improved sustainability and greater resilience against climate change. Grass-based feeds are required that deliver economic and high quality fodder for the grazing animal and safe, healthy and nutritious animal products for the customer. In addition to improved grass quality, safeguards are needed that will increase persistency and resilience to factors that may impair optimum growth or, in the worst case, survival; a likely consequence following onset of biotic or abiotic stresses or of climate change.

The genetic diversity in grass ecotypes provides us with a rich source of novel gene combinations available for use in our plant breeding programmes. For example, the incorporation of genes for water or nutrient use efficiency from fescues in high quality ryegrass cultivars will make grassland production more economic and provide environmental benefits. In this way we are able to respond to requirements for more efficient water use and improved soil and water quality without compromise to the maintenance of an attractive landscape or an efficient agricultural output (Figure 2.1).

In addition to forage grasses, amenity grasses will be tailored to meet the demands of customers such as local authorities, landscape contractors or private leisure and sporting organisations. Turfgrass is an important, if unobtrusive, part of our lives with functional (erosion control; reduction of glare, noise, heat build-up and air pollutants; stabilising dust and soil), recreational (sport and leisure, Figure 2.2), and aesthetic/psychological benefits.

The GTV programme provides a holistic approach to grassland research involving collaboration with other sections of IGER. Work will incorporate the

![Fig 2.1 Contributing to sustainable farming in the UK](image)
impacts of new cultivars on biodiversity of the whole grassland ecosystem, including microbes within the soil and also those within the rumen of the grazing animal (with implications for the health of the feeding animal and its ability to provide safe and nutritious food for mankind). New research priorities include the design of grasses with traits to counter flooding, severe drought, soil-erosion, etc., or as providers of environment-friendly alternative supplies of renewable energy, or for bioremediation of heavy metals and atmospheric pollutants.

A close association with our commercial partner, Germinal Holdings, enables the development and marketing of IGER grass varieties. In turn, IGER supports the UK grass seed industry by producing award-winning forage grass varieties including ‘AberDart’ (a high-sugar grass for improved nitrogen use efficiency and reduced N pollution) and amenity varieties such as the novel wear-tolerant variety ‘AberImp’. IGER fodder grass varieties now account for 39% of UK grass seed production.

New developments and technologies
The GTV programme aims to employ efficient, precision, marker-based selection technologies that ensure a genotype design offering a predictable and desirable phenotype. This is achieved by assembling a precise genome constitution representing a range of selected target traits in experimental breeding lines, and subsequently monitoring their transfer over generations into marketable new varieties. New developments make this possible.

A range of trait ‘dissection’ and mapping technologies of differing specificity are available. These include the use and development of new genetic maps in perennial ryegrass or meadow fescue where, for example, quantitative trait loci (QTL) for key traits are assigned to their respective chromosome locations for each species.
QTL are locations within the genome (ultimately, genes) which, acting in combination, define a trait. QTL analysis requires the construction of a mapping population and chromosome maps on which the positions of large numbers of molecular markers are precisely known. Whilst this provides clues as to the chromosome location of genes concerned with expression of complex traits, it has limited usefulness. Other more targeted approaches are also used within the GTV programme. One, termed introgression-mapping, involves gene transfer (by conventional crossing) from fescue species into ryegrass. Fescue genes that convey ‘sustainability traits’ are used to replace their less-efficient ryegrass equivalents. Ryegrass genotypes with fescue genes are being exploited in cultivar development. Genotypes are selected that contain single fescue chromosome segments and are tested for fescue-specific traits such as resistance to abiotic or biotic stresses, altered flowering time and intensity, plant size, root development, or adaptations that make plants more water- or nutrient-use efficient. Fescue-specific genetic markers aligned closely to the target genes are then developed in order to monitor their transfer through the plant generations required to produce a new grass cultivar.

An example of the selection of an introgression line and development through to a marketed variety serves as a prototype for further work in this area. ‘AberNile’ was the first ever commercially produced stay-green grass cultivar. The initial work involved the transfer of the ‘stay-green’ trait from meadow fescue into perennial ryegrass. Stay-green is controlled by a single gene ‘sid’. In collaboration with the Molecular and Applied Genetics programme, a ‘breeders’ toolkit’ incorporating markers flanking the sid gene has been constructed enabling the gene to be readily transferred across generations. Similar ‘toolkits’ are currently available or under development for a range of the more complex fescue traits listed above.

A new development in marker-assisted trait selection utilises a highly targeted mapping approach termed ‘association mapping’ or ‘linkage disequilibrium' (LD). This relies on non-random association of genes due to their very close proximity one with another on a chromosome. It is being used to identify diversity in natural populations of perennial ryegrass collected at widely differing locations in Europe to increase QTL resolution and locus allele number. Individual base-pair differences (termed single nucleotide polymorphisms or SNPs) amongst alleles at the same genetic locus can explain differences in plant phenotype and, as such, SNPs...
provide the most robust of gene markers for marker-assisted selection and for introgression breeding programmes. SNPs in candidate genes associated with water soluble carbohydrates (WSC) and flowering time are being investigated as proof of principle. As an example of exploiting the wide genetic variation inherent in highly heterogeneous perennial ryegrass populations, a large number of SNPs were identified at the alkaline invertase (an enzyme involved in carbohydrate metabolism) locus in genotypes taken from diverse locations. Comparative mapping, employing model crops such as rice, has provided candidate genes for LD studies associated with flowering and stress resistance, and in some cases these are at the same location as QTL. For example, an alkaline invertase gene on chromosome 6 was associated with a WSC QTL, and dehydrin genes (to avoid cell dehydration) on chromosomes 4, 5, and 6 also corresponded precisely to the location of related QTL for stress resistance.

In addition to IGER-generated developments, international research on monocots indicates similarities in gene order between species (synteny). Despite large variations in genome size and incidences of genome rearrangements, it is becoming clear that the genetic make-up of grasses is inherited from a common ancestral species. This means that there are opportunities for knowledge transfer across species. For example, knowledge of genome structure, and especially gene location, in well researched crops such as rice can be used to predict the location of their allelic variants in ryegrass or fescue species.

Different approaches to gene mapping thus interact closely and enable trait ‘dissection’ and, with gene anchors from the sequenced rice genome, studies of gene synteny across monocot species. QTL analysis, expression studies, and synteny will provide markers (SNPs) for allele identification in natural and experimental breeding populations, use in marker-assisted introgression and selection, and constructive information exchange across monocot species. This will benefit a new BBSRC Cross-Institute Programme (CIP) initiative for studies relevant to all monocot crops.

**Technologies for trait analysis**

In addition to the need for rapid-throughput gene identification, are required for analytical tools that can be used to screen efficiently large numbers of plant samples for the presence of traits of importance for both crop sustainability and for increased agronomic value. New high-throughput technologies for large-scale trait analysis are being explored. For instance, developments in Fourier Transform Infrared Spectroscopy (FT-IR) and associated informatics systems will facilitate future work in this area. We are in a strong position to calibrate FT-IR against well characterised physiological changes in whole-tissue soluble sugar and starch composition and also against variation for carbohydrates in plant populations. In addition, the employment of new proteomic and metabolomic technologies (analysis of the complete protein and metabolite complement, respectively) will demonstrate impacts of IGER grass varieties on the feeding animal and on the environment.

**Conclusions**

Forage and amenity grasses for the future must not only utilise resources (i.e. nutrients and water) more efficiently but also confer measurable benefits in terms of environmental quality. To help achieve this, new biotechnological approaches such as functional genomics, marker-assisted introgression/selection and transgenics or small interference RNA (siRNA) for gene silencing (to confirm gene function) are becoming more accessible. However, informed use of biotechnology requires basic knowledge of relevant traits and their genetic, biochemical and physiological characteristics. This will be the priority for future GTV research.

**Contact:** mike.humphreys@bbsrc.ac.uk