Invited Commentary

Exploring genomes in agriculture and food science

The way in which food is produced, processed and delivered to the consumer is the concern of farming and industry worldwide. The desire to produce nutritious food more efficiently has led to the increasing use of advanced molecular technologies in nutritional sciences (van der Werf *et al.* 2001). This area of research can be considered to fall within the emerging science of nutritional genomics. Whilst the focus of nutritional genomics has been human health (Stover, 2004), its utility is now beginning to extend beyond the study of human systems to include agriculture and food science.

The significant advances made within the field of nutritional genomics have been underpinned by the advent of genome sequencing projects, which has led to an explosion of available genetic information. Genomics involves the study of genes and their functions in an organism. It aims to understand the structure of the genome, including the mapping of genes and the sequencing of DNA. However, the realisation that the genome sequence fails to explain the fundamental nature of many biological processes has led to the development of post-genomic strategies (transcriptomics, proteomics and metabolomics) aimed at relating gene expression to phenotypic outcome.

Transcriptomics monitors the expression levels of thousands of genes simultaneously at a specific time and set of conditions and permits the characterisation of mRNA populations. This ability to determine gene expression on a global scale has been facilitated by the development of high-throughput platforms such as DNA microarrays and related technologies. Proteomics complements and extends the study of genomes and transcript data, reflecting the true biochemical outcome of genetic information. Proteomics may be defined as the study of the protein component of a cell, tissue or organism at a given time under given conditions (Wilkins *et al.* 1995) and has progressed from the simple identification of proteins to studies that are concerned with protein quantification and proteome dynamics. Proteomic analyses require a combination of efficient and stringent separation technologies and high-resolution MS.

Metabolomics is focused on the analysis of low-molecular-weight metabolites, which are the endproducts of gene expression and are regarded as important indicators, and indeed, integrators, of phenotype (Whitfield *et al.* 2004). Metabolomics represents a radical shift from single metabolite monitoring to complex metabolite profiling and pattern recognition. A major goal of modern metabolomic strategies is to measure each individual metabolite within a biological sample. The wide range of low-molecular-weight metabolites in complex biological systems demands a variety of analytical platforms for detection, identification and quantification of

molecules with diverse chemical and physical properties. Suitable techniques that are sensitive, robust and have the capacity to acquire data on large populations of metabolites include MS and NMR spectroscopy.

Since nutrition plays a crucial role in the development of human diseases the focus of many nutritional genomic studies to date has been the investigation of the relationship between genes and diet and how these interactions may impact on human health (Ordovas & Mooser, 2004). The manifestation of nutritional deficiencies or disorders such as diabetes, CVD and obesity is known to be influenced by diet. Therefore determining the composition of foods and understanding how food components can modulate health may prove important in the management of these diseases. Nutritional genomic strategies will be useful in providing molecular biomarkers of health and disease and in understanding gene expression changes induced by whole diets or individual dietary constituents (Kussmann *et al.* 2006). This has evolved into the concept of personalised nutrition, which offers the possibility of tailoring dietary recommendations and more effective management of diseases (Watkins *et al.* 2001).

In the present issue of the *British Journal of Nutrition*, Brown & van der Ouderaa (2007) discuss the applications of nutritional genomics to agriculture and the food industry. The review outlines how investigators are now using nutritional genomics to identify crops with desired genetic characteristics and to enhance the nutritional quality of plants (DellaPenna, 1999). These approaches have previously been employed to produce GM crops and to profile their molecular composition (Kuiper *et al.* 2003; Cellini *et al.* 2004). The authors also describe the use of these technologies as part of selective breeding programmes of livestock (Georges, 1999). The focus of these studies is an understanding of the genetic basis of commercially important traits of farm animals such as reproductive health, disease resistance, growth, fat deposition and milk production. The ability to predict such traits is of immense value to agriculture and food production and there is a clear role for nutritional genomics in developing the knowledge obtained from these studies.

Nutritional genomics has also influenced the monitoring of food composition, authenticity and safety, a key area for the food industry. Nutritional genomic strategies are increasingly being employed to confirm the origin and source of food ingredients (Popping, 2002) and feed products (Fernandez Ocana *et al.* 2004). These technologies are powerful tools with which to detect food allergens and evaluate changes in plant- and meat-based foods upon processing (Carbonaro, 2004). They can also be used to evaluate meat quality (Bendixen, 2005; Mullen *et al.* 2006), and provide a means

of identifying markers of food spoilage in fruits, vegetables, meats and dairy products (Brul *et al.* 2006).

Genomic, transcriptomic, proteomic and metabolomic strategies are making a significant impact on the landscape of agriculture and food technology. The genome sequences of a number of agriculturally important plant species such as rice and farm animals including the pig, cow and chicken have been obtained or are well advanced. Further, public resources such as ARKdb (Hu *et al.* 2001) and AgBase (McCarthy *et al.* 2006) now exist for the functional analysis of genes and their products in numerous animal and plant species. The genetic manipulation of plants and animals for higher nutritional quality through nutritional genomics may benefit crop and livestock management, leading to more efficient production methods and improvements in diet and health.

Whilst this technology is advancing rapidly, challenges remain and nutritional genomics will be best addressed by integrative studies that include measurements of mRNA, proteins and low-molecular-weight metabolites over time and under varied conditions. Understanding these complex networks will require bioinformatics to obtain additional insights and provide the opportunities for greater exploitation of this information. Whilst this goal may currently be elusive, the umbrella discipline of nutritional genomics has the potential to make a significant impact in the way that we view the availability, production and, ultimately, personalisation of our dietary needs.

Phillip Whitfield

Proteomics and Functional Genomics Research Group
Faculty of Veterinary Science
University of Liverpool
Liverpool
UK
p.whitfield@liverpool.ac.uk

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