

The development of 'omics technologies and the food sector

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Over the past 20 years or so huge progress has been made in the sequencing of the genomes of a number of different organisms. At the same time significant advances have been made in the development of analytical approaches and bioinformatics tools to analyse the different cell products, including proteins and metabolites. The disciplines that have arisen from this work include:

- Genomics – study of the gene pool.
- Transcriptomics – study of gene expression (not all genes are expressed all the time).
- Proteomics – study of the protein pool (not all genes expressed are translated into proteins).
- Metabolomics – study of the metabolite pool.

Genomics

The term genome is used to describe all the genes in an organism. The genome is not influenced by either cell type or internal or external changes. The development of large scale DNA sequencing technology has rapidly advanced the field of genomics – the study of the genes in an organism.

This discipline is focused on sequencing the DNA in an organism to form a complete picture, and then identifying specific genes in that sequence which could be of interest. However, genomics does not provide a picture of how the cell/organism actually functions. To do this one must look to transcriptomics and proteomics.

Example:

Fera scientists are looking at how anaerobic digestion (AD), the process of degrading waste to produce biogas, can be used to deal with food waste. AD is a biological process, relying on a complex community of microbes to degrade the organic fraction of food and generate methane. The process can be carried out on an industrial scale. Using DNA sequencing methods Fera scientists are looking at the makeup of these

microbial communities. This approach relies on newly available DNA sequencing technology to generate sequences from all the organisms present in a sample, a technique called metagenomics. For example, it is possible to generate sequences from the complex communities of AD and identify which micro-organisms are present, and which are correlated with particularly efficient or inefficient digesters. Strategies can then be devised for better monitoring and operation of AD systems to convert food waste to biogas with maximum efficiency.

Transcriptomics

The transcriptome is the complete set of mRNA transcribed from the genome (DNA) in a cell. A cell makes mRNA as required; therefore the amount and type of mRNA present at any time is affected by factors that may influence the regulation of this transcription. The process of transcribing genes into mRNA is known as gene expression. Transcriptomics is the analysis of the genes that have been expressed in a cell. Studying the expression profile of a gene can provide information on its role in a cell.

Example:

Fera is not directly involved in this area. However, an EU-funded, five-year project called 'BioCop', in which Fera is a partner, has a work package looking at how transcriptomics can be used to look at monitoring for chemical contaminants in foodstuffs. One of the main features of this approach is that it will enable the assessment of cumulative effects of multiple food contaminants on individual biological pathways.

Proteomics

The proteome is the complete set of proteins that can be produced by a cell/organism at any given time. The amount of any protein produced depends on the gene it is transcribed from and on the physiological state of the cell. Cells respond to internal and external changes by adapting the level and activity of proteins they produce.

Proteomics is the study of all of these proteins. Proteomics does not simply study the proteins themselves, but also their interactions, any changes they undergo, and the effects that they have within the cell.

As proteins are involved in almost every cellular process, proteomics can provide a comprehensive picture of a cell's state. Proteomics can also confirm the presence or absence of a specific protein and the amount present.

Example:

Fera researchers have worked with the University of York to investigate if proteins from a different species had been added to chicken. This is important because the species must be clearly marked on the label. By using proteomics the researchers were able to look for non-chicken peptides in chicken products, something that would not be possible using DNA-based methods. Fera's proprietary database of peptide sequences provided the necessary species specificity.

Analysis of both commercial injection powders and catering packs of chicken fillets indicated that proteins from beef or pork gelatine were present in some samples.

Gelatine may be added in 'injection' or 'tumbling' mixtures used to help retain water in chicken breast products. Although use of these non-chicken proteins does not make chicken products unsafe, it is important that people are given accurate information about what is in their food. For example, the presence of meat products in poultry is of major religious and ethical concern in relation to halal and kosher products.

Metabolomics

The metabolome consists of all the likely small molecule metabolites that can originate from cellular processes.

Metabolomics is the study of changes in concentration, interaction and location of these metabolites i.e. the metabolite profile. This profile can be used to describe the physiological state of a cell/organism and its responses to genetic and environmental changes.

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Example:

Scientists at Fera have used metabolomic techniques to identify beef labelled as 'matured'. This labelling is often used as a marketing tool to promote beef as high quality and thus it can be open to abuse. By using a scientific technique called NMR (nuclear magnetic resonance) the metabolite profile of an extract of the meat was used to determine its age and storage conditions.

This is possible because there are systematic changes in metabolite concentrations with age and the rate of these changes is dependent on storage conditions.

The scientists were also able to identify

specific markers indicative of poor storage.

The use of proteomics and metabolomics offers great opportunities to food industry quality control teams.

The 13th Fera/JIFSAN Symposium in June will bring together industrial stakeholders, academic and government scientists to explore the potential impact of these 'omics technologies in the food sector.

They have been at the forefront of biotechnology in the health, pharmaceutical and crop science sectors. However, the potential for their use in the food sector is still largely unrealised.

For more information on the Symposium see www.defra.gov.uk/fera/jifsan2012 ■

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