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Commentary

Functional on Genomics, Proteomics, Metabolomics - Stem Cell

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INTRODUCTION

Nutrigenomics has been defined as the application of a range of the so-called omics techniques (including genomics, transcriptomics, proteomics, and metabolomics) to the field of human nutrition, especially the relationship between nutrition and health. Since 2004, NuNZ has applied nutrigenomics techniques to a variety of studies, using human Inflammatory Bowel Disease (IBD) as a proof of concept. The long-term goal of the NuNZ programme 'Tailoring New Zealand Foods to Match People's Genes' is to develop foods that can be matched to individual human genotypes to benefit the health of specific genetic sub-groups. Over the course of its existence, NuNZ has completed numerous studies using mouse models of IBD, in which a range of omics techniques have been applied, including transcriptomics, proteomics, metabolomics, and analyses of the intestinal microbiota. More recently, some of these techniques have been applied to samples derived from human dietary intervention studies investigating the anti-inflammatory potential of foods or diets.

In the field of nutrigenomics, there are three major applications of metabolomics which are of particular relevance. The first application is to establish as complete a profile as possible of all compounds present in individual foods. This can be relevant when considering which nutrient or combination of nutrients might be contributing to a particular effect of the food in question.

Perhaps the most unexpected use of genomics has been its use as a counting device for DNA and RNA, furthering the study of molecular biology at a systems scale. Apart from counting RNA by converting them into DNA, genomics also has been instrumental in characterizing genomic protection by proteins that control which regions of the genome are active. Sensitive measurement of RNA has enabled catching RNA polymerases in the act of transcribing the genome. Research in our Department has pushed genomics beyond usual molecular biology applications by developing methods to sensitively measure enzyme activity in single cells. Our department is at the cutting edge in developing genomic technologies with applications ranging from structural epigenomics to how RNA modifications affect the aggressiveness of a cancer cell, to RNA stability, function, and structure.

DNA has the blueprint of life. Enumerating the bases that make up the genomes of all organisms continues to be a monumental effort in biology, in a quest to understand life better. The ability to read out sequences cheaply and in a massively parallel manner has changed the way we do biology. Fundamentally, it gives us the ultimate picture of our makeup and our relationships with all the other species. Genomes are a snapshot of evolving species, helping us understand the evolutionary processes and adaptation. Mutations lead to many human diseases. Sequencing can not only help diagnose diseases, but also aid in understanding the molecular mechanisms underlying disease states.

Metabolomics 'aims to profile all the small molecule metabolites found within a cell, tissue, organ, or organism and use this information to understand a biological manipulation'. Importantly, metabolomics analysis can be achieved using relatively non-invasive approaches, for example studying metabolites found in urine or plasma.

The proteome is the set of all proteins produced by an organism or a system. The goal of proteomics has been described as 'a comprehensive, quantitative description of protein expression and its changes under the influence of biological perturbations'. Thus, the study of proteomics comprehensively examines the protein composition and abundance in a given cell population. In the studies NuNZ has undertaken, we have used differential in-gel expression, in which samples from different treatment groups are labelled with different cyanine (Cy) dyes (e.g. Cy2 for animals on a 'control' diet and Cy5 for those which have received a food treatment) and the proteins from both samples are separated on the same gel by 2D electrophoresis. Protein features which were differentially expressed between the treatments are then identified by Liquid Chromatography-Mass Spectrometry (LC-MS) analysis of peptides derived from the differentially expressed proteins.

Mitochondrial mutations may exert unfavorable effect on neuron synapses which may lead to the loss of motor functions causing seizures. Mitochondrial displacement loop (D-loop) is

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the hotspot for mtDNA alterations which influence the generation of cellular Reactive Oxygen Species (ROS). Lack of cellular energy (ATP) due to defective Oxidative Phosphorylation (OXPHOS) and ROS can cause somatic mutations in mtDNA. The concern of the present study is to understand the mitochondrial basis of the disease in our population by identifying the Novel mitochondrial mutations which in turn may facilitate the diagnosis of a section of Juvenile Myoclonic Epilepsy (JME) patient's thereby better management of the condition.