Metabolomics and Individual Metabolic Assessment: The Next Great Challenge for Nutrition

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The human genome has arrived. The technologies of global transcriptional analysis are building the greatest knowledge base in the history of biological science and the world is waiting impatiently for the benefits that this knowledge will provide. Discouragingly for nutrition, in the current public health environment, knowledge from genomics alone will not provide dramatic benefits to quality of life for most people immediately. The genome and its application through functional genomics are building knowledge most rapidly to identify the causes and complications of diseases and resolve them through therapeutic intervention. Nutrition, however, has a broader and more comprehensive mandate than ameliorating disease. Nutrition now arrives at the genomic era with the goal to go beyond curing disease in afflicted individuals, to preventing disease and improving health of entire populations. Nevertheless, nutrition can not succeed in delivering on this bold promise with genomics (the study of entire genomes) as the only tool in its kit. Individuals do not have the luxury of altering their genome during their lifetime. Although genomics will be the essential foundation of knowledge, it is the expression of the genome both as the proteome (the study of entire protein complements of cells tissues or fluid compartments), and more directly as the metabolome (the study of entire metabolite complements in cells, tissues or fluids) (1–3) that will serve as the information base for modern nutrition. The comprehensive study of metabolites will provide nutrition with the tools to enter the ‘omic revolution. In fact, metabolomics should be led by the field of nutrition. For this reason, The Journal of Nutrition is soliciting articles advancing metabolomics. The Journal of Nutrition will view metabolomic articles as those articles reporting on metabolites as entire metabolomes or as subsets whose analysis provides enabling technologies, information technologies (bioinformatics) or interpreted data sets from studies designed to contribute to the knowledge of entire metabolomes.

Scientists are in the process of developing the technologies to quantify entire classes of metabolites. With these tools, clinical scientists will be able to build the key databases of metabolites (metabolomes) much as the human genome has created a database for biological scientists around the world. With databases in hand, the role of nutritionists will be to create a database for biological scientists around the world. The comprehensive study of metabolites will provide nutrition with the tools to enter the ‘omic revolution. In fact, metabolomics should be led by the field of nutrition. For this reason, The Journal of Nutrition is soliciting articles advancing metabolomics. The Journal of Nutrition will view metabolomic articles as those articles reporting on metabolites as entire metabolomes or as subsets whose analysis provides enabling technologies, information technologies (bioinformatics) or interpreted data sets from studies designed to contribute to the knowledge of entire metabolomes.

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Emerging technologies. Global gene expression analysis was made possible by a single invention: the gene array. The immobilization of tens of thousands of individual oligonucleotides, all of which can be simultaneously and quantitatively probed in a biological sample made functional genomics an immediately practical scientific field. Companion bioinformatic tools are rapidly emerging to manage, annotate and interpret the massive data sets that are created. Metabolomics does not have the luxury of a single class of analyte nor a single mode of analysis and the field of metabolomics will continue to be driven by technological developments. Several technologies have been used to this purpose including NMR (4), chromatography (5) and mass spectrometry (6). However, each of these technologies has significant drawbacks either in quantitation, scope or throughput. Hence the journal of nutrition encourages authors making significant breakthroughs in the technologies of metabolite analysis to submit to The Journal of Nutrition. Techniques could include the more traditional analytical chemistry tools (NMR, mass spectrometry, various high-resolution chromatographies) as well as newly discovered analytical platforms. Hyphenating chromatographic techniques (GC, HPLC, CZE) to spectroscopic tools (MS, NMR, FTIR) has accelerated compound discovery and with the availability of fast gas chromatography, capillary HPLC and microfluidic technologies, separation science is continuing this evolution. The editors welcome articles describing new break-

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throughs in analytical biochemistry that enable metabolomic analysis and automated management and interpretation.

**Functionally annotated metabolome databases.** The human genome has demonstrated vividly that the evolution of broad unbiased biological databases is the necessary basis of future research and development in all of the biological sciences. An important conclusion from the initial studies is that databases are valuable to subsequent investigation if data are quantitatively comparable. The value of a single gene expression experiment is minor in isolation. The ability to compare date (data mining) and to search intelligently using modern bioinformatics tools is driving a new dimension of knowledge building. Similarly, establishing quantitative databases of metabolic data that can be polled and interpreted independently is now an objective of modern nutritional science. It is because the human genome information is integrated into a single data resource that grows in size and value with time that it is so valuable to discovering the role of genes in human biology. As there is no analogous resource for metabolism, there is a pressing need for *The Journal of Nutrition* to coordinate the scientific fields needed to generate, annotate and mine metabolome databases. *The Journal of Nutrition* will house the dialogues necessary to define the suitability of data and how it is produced and reported, allowing the seamless integration of all data into comparable databases. The editors of *The Journal of Nutrition* invite authors to submit articles describing and interpreting large metabolic databases emerging from high-throughput biological analyses of animals and humans.

**Interaction of environment and metabolism.** The traditional approach to understanding the effects of environment, i.e., nutrients on metabolism, is to study the effects of single nutrients on single biological reactions, enzymes, genes, etc. The single effects of nutrients have to be gradually assembled into an integrated picture, but performing the necessary analyses simultaneously within a single experiment was previously beyond the scope of traditional nutrition research. The single effects of nutrients have to be gradually assembled into an integrated picture, but performing the necessary analyses simultaneously within a single experiment was previously beyond the scope of traditional nutrition research. The ability to compare data (data mining) and to search intelligently using modern bioinformatics tools is driving a new dimension of knowledge building. Similarly, establishing quantitative databases of metabolic data that can be polled and interpreted independently is now an objective of modern nutritional science. It is because the human genome information is integrated into a single data resource that grows in size and value with time that it is so valuable to discovering the role of genes in human biology. As there is no analogous resource for metabolism, there is a pressing need for *The Journal of Nutrition* to coordinate the scientific fields needed to generate, annotate and mine metabolome databases. *The Journal of Nutrition* will house the dialogues necessary to define the suitability of data and how it is produced and reported, allowing the seamless integration of all data into comparable databases. The editors of *The Journal of Nutrition* invite authors to submit articles describing and interpreting large metabolic databases emerging from high-throughput biological analyses of animals and humans.

**Integrated metabolite databases.** The human genome project demonstrates the value of building comprehensive and integrated databases for the purpose of discovery. Were the gene data generated from individual researchers to remain discrete and not integrated or compared with this larger resource, the value of individual experimental results would, of course, be greatly diminished. There is at present no analogous single resource database for metabolism, making it impossible to take comparative advantage of the myriad scientific investigations examining variations in human and animal metabolism. No central data repository is currently positioned to accept raw metabolite data. Nevertheless, straightforward practices can ensure that the data produced presently can be integrated into future integrated metabolome databases. All data produced and reported should be quantitative and not relational, thereby allowing their seamless integration. By determining the quantitative concentrations of each target metabolite in a system, comparisons are independent of the number of metabolites measured, and are additionally independent of the analytical platform that produced the data. Furthermore, quantitative metabolic data are interpretable on the basis of the true molar relations among all the metabolites measured using highly multivariate statistics.

The more subtle and broad effects of food on metabolic regulation and tissue composition provide nutrition with both a challenge and an advantage in delivering health to individuals at risk for complex or chronic diseases. Given a proper understanding of the effects of food on metabolism, diet can modify individual metabolic regulation in a broad and likely highly controllable fashion. Lowering the risk of one disease provides little health advantage if in so doing the risk of others is increased. Therefore, integrating metabolism broadly in response to dietary intervention is a necessary element of preventative nutrition. *The Journal of Nutrition* encourages the submission of articles that describe metabolic regulation from the complete, metabolomic perspective in response to nutritional intervention, particularly articles that integrate genomic and transcriptomic data to complement metabolomic data. The initiative that *The Journal of Nutrition* has undertaken is designed to produce the tools, legacy databases and understanding necessary for the field of nutrition to continue on its path as the reservoir of integrative science, building scientific knowledge from the cell and molecule to the whole body and beyond to populations.

**LITERATURE CITED**