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Nutrient-Gene Interactions: Knowledge to Action within an IUNS Task Force

Personalized nutrition is becoming a globally important area not only for clinical purposes and research, but also for wide-ranging health maintenance interests that should complement knowledge and actions concerning public health nutrition issues. The application of modern technologies such as the Internet and mobile phones, individually oriented anthropometrics and biochemical measurements, advanced customized phenotypical biomarkers directed to assess newer hormonal, inflammatory or stress signatures, last generation 'omics' approaches and genome-related information are relevant topics for a balanced progress and acceptance of personalized nutrition matters.

In this context, personalized nutrition would be based on the principle that the quantity and quality of consumed foods or an individual's nutrient requirements associated with the genetic make-up may represent risk or protection factors for various diseases, where outcomes depend on the ability to regulate the expression of genes and on the genetic make-up. The interplay of personalized nutrition relies on the genetic background (e.g. heritage or epigenetic markers), the preferences of the individual (physical activity, attitudes, likes and dislikes, etc.), genetically regulated biological functions (appetite, digestion, metabolism, etc.) or unique clinical characteristics (family medical background, personal history of diseases, intolerances and allergies) and cultural variation (e.g. food customs, religion and food accessibility). Indeed, cell functions are regulated in an orchestrated way by genes involving all homeostatic pathways in the body through the nucleotide DNA code and its associated single nucleotide polymorphisms (SNPs), mRNA expression patterns, epigenetic machinery, etc. Overall and despite the fact that some discrepancies concerning the meaning and contents of the discipline of nutritional genomics still exist, it is assumed that this science involves an 'omics' approach (e.g. transcriptomics, proteomics, metabolomics and microbiomics) to explain how food/nutrients and genetic material interact and how genes are expressed to drive individual phenotypes. This scientific field also includes research in nutrigenetics, nutrigenomics, nutriepigenetics and systems biology strategies. Thus, nutritional genomics can contribute crucially to personalized nutrition implementation, to the development of reliable biomarkers, to the prognosis of dietary responses or to achieving individual nutritional demands.

In addition to genotype-based prescriptions implicating inborn errors of metabolism such as phenylketonuria, lactose intolerance or familial hypercholesterolemia, a relevant and tangible example of the applicability of nutritional genomics is obesity and its accompanying side effects. In this sense, the occurrence of SNPs, which consist in replacing a single nitrogenous base in a nucleotide of DNA that occurs in at least 1% of the population, may affect the synthesis and functions of specific proteins and, therefore, may alter nutritional requirements and nutrient metabolism. One hypothesis for the great variability in the diet response would be the genetic variability. Some SNPs in obesity candidate genes, e.g. PPAR-gamma, UCPs, ADBRs, PLIN-1, TCF7L2, FTO, LEPR or MCR4, affect the weight loss outcome in genetically predisposed subjects and interact with the energy and macronutrient content of the dietary prescription. In addition, SNPs in genes encoding inflammatory markers have also been related to lower or higher rates of success in the obesity treatment. Indeed,

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there have been reports about a number of cases where the allelic distribution of obesity risk genes influences the outcome of energy restriction or the response to a variation in the macronutrient composition of a hypocaloric diet.

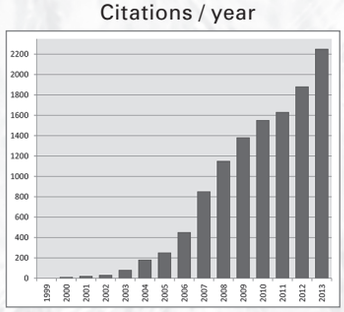
Interindividual differences in obesity susceptibility depend not only on the DNA sequence (e.g. SNPs), but also on epigenetic factors affecting gene expression such as DNA methylation, covalent histone modifications, chromatin folding and the regulatory actions of miRNA and polycomb complexes. The identification of those individuals that at an early age could present changes in the methylation profiles of specific genes could help to predict their susceptibility to develop obesity and related comorbidities later, which may allow to prevent and follow up the progress as well as to research and develop personalized therapeutic approaches. Tailored dietary treatments in the perinatal period are of interest and value to neutralize putative adverse epigenomic events related to the onset of adult chronic diseases in later life.

There are some challenges concerning nutritional genomics and its application in nutritional prevention and treatment. One of them is that most of the SNPs differ in importance depending on the ethnic background, so even more studies with large and/or mixed populations and with different ethnic subgroups are required. The cost of genetic analyses and personalized advice must go down in order to extend the use of nutritional genomics to public health and clinical practices, which is starting to be achieved with newer and lower-priced sequencing and microarray platforms. Furthermore, clinicians, dietitians and other health professionals must be familiar with the genetic information provided by direct-to-consumer tests and should be able to translate the genetic results into personalized nutrition. Indeed, the development of bioinformatic tools is a key point to improve genetic data interpretation. Also, continuing education at the undergraduate and postgraduate stages for health trainees should be promoted. Another important issue is the consideration of the ethical principles that are to govern the management of this very sensitive information, involving genetic markers as well as the legal regulations to be applied at a national and universal level. Actually, concrete regulatory norms and guidelines and the provision to consumers of better information about the benefits and limitations of using nutritional genomics devices are still not available.

Generally, the promotion of scientific events in the nutritional genomics area and the narrowing of existing consortia/societies concerning this field, such as the Nutrigenomics Organisation (NuGO) and the International Society for Nutrigenetics and Nutrigenomics (ISNN), must also be encouraged. Interestingly, IUNS has had a Task Force since 2005, devoted specifically to this endeavor, named Gene-Nutrient Interactions: Knowledge to Action, while two journals Genes & Nutrition (Springer) and Journal of Nutrigenetics and Nutrigenomics (Karger) express this scope in their titles. The number of publications/articles related to nutritional genomics and their associated branches such as nutrigenetics and nutrigenomics are continuously evolving (nearly 1,000 documents with more than 12,000 citations since 2001), which is paving the way for successful and efficient progress in the field of personalized nutrition.

Helen Hermana M. Hermsdorff
Department of Nutrition and Health, Universidade Federal de Viçosa, Viçosa, Brazil

J. Alfredo Martínez
Department of Nutrition, Food Science and Physiology, University of Navarra, Pamplona, Spain
CIBER Fisiopatología Obesidad y Nutrición (CIBERObn), Instituto de Salud Carlos III, Madrid, Spain



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