Understanding Nutrigenomics and its Practical Applications

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The integration of genomics into food and nutrition applications has begun. The process is expected to impact virtually every subdiscipline of dietetics, from food science and nutrition science research to clinical nutrition interventions to the development of functional foods and dietary supplements. This emerging field of study is called nutritional genomics, or nutrigenomics.

Genes provide the information that’s translated into how we look, how we function. In nutrigenomics, the focus is on how genes affect our ability to extract, absorb and use bioactive components in food to support life and the ability of these bioactives to influence the expression of our genes.

Nutrigenomics research is expected to continuously move us closer to defining the best match between our food choices and or genetic makeup or genotype), providing a solid foundation upon which to base diet-related disease interventions and health promotion approaches. Panels of genetic markers will identify which individuals will respond favorably or unfavorably to particular dietary approaches. As with the need to match drug therapy to an individual’s genotype (pharmacogenomics), it is important to match food components to our genes in order to achieve maximal effectiveness and to avoid negative consequences that can occur when the environment is at odds with the individual’s genotype. Dietary components, as functional foods or dietary supplements, will be used to increase or decrease the expression of particular genes to improve health.

The impact of nutrigenomics will extend far beyond the obvious clinical nutrition applications, however. Equally important will be the applications to food science and the development of health-promoting foods, the need to educate consumers and professionals about this new science, and the development of nutritional standards for different populations. Virtually every aspect of dietetics will be affected. For reviews of nutrigenomics and perspectives about its anticipated applications, see references 1-13.
As I write, we are celebrating the first day of spring! What a wonderful time – a time of birth, growth, new beginnings, and renewals of all kinds. It is my wish that we hold on to the joy of this time all year long.

Likewise, this is also a symbolic new beginning for NCC. We have had a great year with a healthy growth in our membership and (very exciting), the official positioning of NCC as the home of nutrigenomics! And it won't stop there…our Executive Committee is hard at work planning for our upcoming strategic planning event – a time to brainstorm for the future growth and successes of this fine group. As we welcome our members’ input on all issues and ideas I encourage any of you with specific input to contact me at sallen947@sbcglobal.net or (630) 853-8891 or any board member listed on the back of the newsletter.

Bittersweet, I must bid you adieu as Chair as my term transcends to Past Chair as of June 1st. I gladly hand over the reigns to Douglas S. Kalman MS, RD, FACN and of course, will remain very active and supportive of NCC in my final leg of officership.

In line with new beginnings, I offer congratulations to our newly elected officers, Gretchen Forsell MPH, RD, LMNT as Chair Elect, Andrea M. Hutchins PhD, RD as Treasurer; and Jessica Lane MS, RD, Kathy Moore RD, LD, CCN, and Sarah O’Brien MS, RD for Nominating Committee. We welcome each of you and look forward to your expertise and valuable contributions.

Lastly, aloha to Hawaii! We hope all of you will be taking advantage of the amazing opportunity to combine work and pleasure at this year’s FNCE. Wait until you see what NCC has in store for its members! A special opening night celebration that NCC members will be a special part of, an afternoon educational tea, two exciting NCC sponsored FNCE sessions, and once again this year, rejuvenating yoga. What ever you do – try not to miss this one!

In closing, I have no doubt that NCC will continue to be one of ADA’s premier dietetic practice groups. I personally will do whatever I can to support this effort as I hope is the same thought each and every one of you has as well. Together, we'll ride the tide into the future. How bright, how exciting – just like the spring sun!

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Genetic Principles

A brief discussion of the basic principles underlying nutrigenomics is helpful in understanding the potential applications. For background information, see the review by Kauwell1, introductory genetics and human genetics textbooks,14-17 Genetics: the Nutrition Connection,18 It’s Not Just Your Genes,19 and the nutrigenomics postings on the NCC web site.

DNA is the genetic material, a molecule that carries information encoded within its linear arrangement of nucleotides. A gene is a sequence of DNA that directs the synthesis of a protein. Proteins perform the work of cells and function in a variety of ways: as an enzyme, receptor, transporter, communicator, hormone, or regulatory factor. Many genes influence or are influenced by environmental factors, such as the bioactive components found in food (nutrients and non-nutrient components, such as phytochemicals). Either the protein coded for by the gene influences the ability to use (digest, transport, metabolize) particular bioactive food components or the expression of the gene itself is influenced by certain bioactives.

Changes can occur within the genetic material. Because DNA is an informational molecule, any change can potentially alter the outcome when DNA is converted to protein. In some cases changing the base component within a single nucleotide [A (adenine), C (cytosine), G (guanine) or T (thymine)] leads to major dysfunction. Well known are the inborn errors of metabolism, such as phenylketonuria and galactosemia. This classical application of genetics to nutrition practice is one in which dietetics professionals have long played a valuable role. Advances in nutrigenomics now permit practitioners to focus on genetic changes that alter function less dramatically, as well as those that are expressed within certain environments. Although all of these changes—major and minor—are technically mutations (changes in the DNA), there is a preference among those in the field to refer to the major changes as mutations and the minor ones as genetic variations or gene variants.

Presently the type of gene variant most relevant to nutrigenomics is the single nucleotide polymorphism (SNP, pronounced “snip”). A SNP by definition is common within a population, occurring in >1% of the individuals. The change may be a single base change or the loss or addition of a limited number of bases (micro-deletion/micro-addition). SNPs serve as markers for genes, or a way to detect the presence of the change in DNA. Changes may occur in the coding region of the gene, in its promoter (regulatory) region, or be physically close to the gene but not actually within it.

Nutritional Genomics vs. Nutrigenomics vs. Nutrigenetics

Unfortunately, confusion in terminology often accompanies the emergence of a new discipline. The term nutritional genomics refers to the discipline itself and is frequently shortened to nutrigenomics. It is also used to describe the impact of bioactive food components on gene expression—the mecha-
isms by which the communication process takes place and by which gene expression is altered by food components. Nutrigenetics concerns how an individual's genetic makeup (genotype) affects the ability to process and use food, which determines the nutritional requirements for that individual. So, nutrigenetics focuses on the impact of genetic variation on the ability to use food to supply optimal nutritional needs. Both describe diet-gene relationships. The decrease in expression of inflammatory-promoting genes by omega-3 fatty acids is an example of nutrigenomics. The increased requirement for folic acid by individuals with a particular variation of the 5,10-methyltetrahydrofolate reductase (MTHFR) gene is an example of nutrigenetics.

Just like a focus on genetics preceded the current emphasis on genomics, nutrigenetics will be the focus of the early work integrating genetics into food and nutrition. For further discussion of nutrigenomics vs. nutrigenetics, and of genetics/genomics as applied to nutrition, see the review by Ordovas and Corella and the nutrigenomics postings on the NCC website.

The State-of-the-Science

Common to both nutrigenetics and nutrigenomics is the importance of developing an extensive body of research from which practical applications will evolve. Key issues that are being addressed include:

• identifying which genes are diet-responsive and to which bioactive food components;

• understanding the mechanisms by which these components communicate with the genetic material and the proteins and other molecules involved;

• identifying which foods are rich sources of each major bioactive;

• identifying gene variants of each diet-responsive gene and its impact on function;

• developing and validating diagnostic tests that detect those gene variants known to impact response to diet;

• surveying populations and identifying which gene variants are most prevalent, which thus defines the most prevalent disease risks;

• developing nutritional guidelines for intervention in the case of dysfunction that has already developed;

• preventing disease from manifesting in individuals known to be susceptible; and

• converting these research findings into practical applications for customized nutrition approaches for populations at particular risk as well as for individuals.

Clearly, nutrigenomics is a science in progress. Not surprisingly, there is controversy surrounding the degree of readiness for application in practice. Central to the controversy is the selection of the gene variants that form the basis for diagnostic tests that alert one to increased risk for developing particular chronic diseases. It’s helpful to establish guidelines for selecting a SNP as a diagnostic marker for nutrigenomics applications. Five criteria include the following:

1. Ideally, the SNP has a measurable effect (change) on function, such as on enzyme activity or gene expression;

2. This change in function is reflected in an effect on a measurable biomarker, such as homocysteine, cholesterol levels, or cognitive ability;

3. The SNP is found to be associated with a state or condition, such as the vitamin D receptor (VDR) gene and osteoporosis or the angiotensin-converting enzyme (ACE) gene and exercise activity;

4. There is a diet-gene interaction. so diet can intervene positively on the effect of the SNP on function and so that, once you identify a person with a particular SNP, there’s positive action that can be taken to better their situation);

5. There is a significant amount of peer-reviewed literature supporting the association of the SNP with this effect on function and its phenotypic outcome.

These standards for SNP selection are goals towards which the field of nutrigenomics is moving. You will find for many SNPs that there are gaps, some minor, some major. You will need to use the scientific literature as your primary source of information in order to stay abreast of developments as the practical applications are finetuned over time.

Genetic Screening for Diet-Related Gene Variants

Screening for diet-related variants is simple and noninvasive. Any cell with a nucleus contains the total complement of DNA and can serve as the test material. The most readily available are the buccal cells that line the inside of the cheek. Using a sterile swab containing a brush-like tip, the cheek tissue is swabbed to collect the DNA sample. The sample is then sent to a laboratory where the DNA is extracted, amplified in amount, and prepared for analysis of the particular DNA sequences of interest. Within 2-4 weeks, a report is received that contains the results of the analysis. Some companies will provide only genetic results and others may include health implications and suggestions for nutrition and other lifestyle changes that can help to minimize the risk of disease susceptibility. Whether the report is sent directly to the individual or to the healthcare professional depends upon the laboratory used.

At the time of this writing, at least six companies offer screening for diet-related gene variants that are associated with disease susceptibility. Such testing is a relatively new service and does not fall under standard laboratory accreditation requirements. However, some companies take great care to ensure that the laboratories they use follow standard laboratory quality.
assurance measures and voluntarily seek certification and accreditation. In deciding among the available testing choices, the following questions can help to determine which options best meet your needs.

- Is the test accompanied by an informed consent form? This form should address how your DNA will be used and how privacy is ensured.
- What happens to your DNA following testing? Ideally you want your sample destroyed and the data not released to anyone without your written consent. There may be an opportunity for your sample and test results to be included in ongoing research. If you wish to participate in such research, your informed consent form should provide the pertinent information and require your written consent.
- Which risks are assessed or which disease susceptibilities are examined?
- Which SNPs are tested?
- What is the scientific documentation associating each SNP to a particular disease?
- For each SNP, is there action that can be taken to reduce risk? If so, what is the scientific documentation for these associations?
- Does the company perform the testing itself? If not, which laboratory is used? What are the credentials of the laboratory? At a minimum, the lab should have quality control procedures in place and many states require CLIA-certification (Clinical Laboratory Improvement Amendments of 1988).23
- Has each test been validated for accuracy and sensitivity? If so, how can you obtain information pertaining to validation?
- What is the minimum age for testing?
- How long does the process take from the time a sample is received until the report is received?
- Is there someone with whom you can discuss the results and their implications? If so, what are the credentials and experience of this individual?

**Examples of Nutrigenomic Applications**

There are many examples within cardiovascular disease that illustrate how nutrigenomics/nutrigenetic approaches are being practically applied. Clinical practitioners have long been aware that individuals vary significantly in their response to dietary therapies designed to change plasma lipid concentrations. The application of nutrigenomics approaches helps to clarify the basis for the inter-individual differences in response and to provide guidance for therapeutic interventions.

There are a number of diet-responsive genes involved in healthy vascular function, and SNP variants have been identified for many of these genes. Using genes that are known to impact serum lipid levels as examples, several clinically useful SNPs include the genes for apolipoprotein E (APOE), apolipoprotein A-1 (APOA1), cholesteryl ester transfer protein (CETP), hepatic lipase (LIPC), and lipoprotein lipase (LPL).

It’s helpful to know the gene variants that an individual has (or that the majority of a population is likely to have) and how these gene variants interact with dietary factors when working with clients for effective ways to lower serum lipid levels. For this article, the APOE gene and its common variants will be used as an example of how the practitioner might use nutrigenomics to customize dietary advice.

A primary role of apolipoprotein E (apoE) is to facilitate the interaction between triglyceride-rich chylomicrons and intermediate-density lipoprotein particles and their respective receptors. The clinically useful SNPs for APOE are three variants (alleles): E2, E3, and E4, with E3 being the most common form. Two amino acid residues are involved in the DNA sequence difference among the alleles. E3 has cysteine at position 112 and arginine at position 158, E2 has a single amino acid change at position 158—a cysteine rather than arginine, and E4 has a single amino acid change at position 112—an arginine rather than cysteine. Individuals can have one of six genotypes: 2/2, 2/3, 2/4, 3/3, 3/4, or 4/4.

A number of studies have examined the interaction between APOE alleles and dietary factors and provided guidelines for dietary therapy. Corella and Ordovas provide an excellent overview in their 2005 review.8 In general, individuals with at least one E4 allele have the highest basal levels of various lipids and show the greatest lipid-lowering response to a low-fat diet. Those with at least one E2 allele have the lowest basal lipid levels and are helped the least by a low-fat diet.

The following summarizes ways in which the presence of either the E2 or E4 allele have been found to influence response to dietary interventions designed to improve serum lipid levels. (Responses are in comparison to the more common E3 allele as the control):

- Those with one or more E2 alleles:
  - have the lowest serum total cholesterol, low-density lipoprotein-cholesterol (LDL-C), and apoB levels of the three APOE alleles;26
  - have the highest triglyceride (TG) levels of the three APOE alleles;26
  - are the least responsive to a low-fat diet;26
  - are the most responsive to oat bran and other soluble fibers;27
  - are the most responsive to endurance exercise26 with an increase in high-density lipoprotein-cholesterol (HDL-C);29 and
• are the most responsive to lowering TGs by fish oil supplementation. 27

• Those with one or more E4 alleles:

• have the highest serum total cholesterol, LDL-C, and apoB levels of the three APOE alleles; 26

• have the lowest basal serum HDL-C levels of the three APOE alleles; 26

• have elevated fasting and postprandial TG levels, though somewhat lower than E2 individuals; 26

• are the most responsive to a low-fat diet; 26

• are the least responsive to oat bran and other soluble fibers; 27

• are the least responsive to the lipid-lowering effects of exercise; 28

• have the least beneficial response to fish oil supplementation (increased total cholesterol and reduced HDL-C); 29

• have increased LDL-C levels when they drink alcohol; 30

• do not increase HDL-C levels when they drink alcohol as is common in those without an E4 allele; 30

• have increased LDL-C levels when they smoke; 31 and

• have increased carotid artery intima-media thickening when they smoke 32.

Just glancing at this list of gene-diet interactions, it is clear that whether an individual has the E2 allele or the E4 allele, impacts diet and lifestyle recommendations for improving vascular health.

Similarly, clinically useful SNPs related to polyunsaturated fat and HDL-C levels (APOA1; 34-37), folate and homocysteine levels (MTHFR; 38-43), hypertension and responsiveness to salt restriction or the DASH diet (AGT; 44-46), as well as a number of other SNPs that influence LDL-C and HDL-C levels have been identified. See Corella and Ordovas for an excellent review of multiple gene-diet interactions and pertinent SNPs. 26

Summary

Nutrigenomics can enhance the assessment of nutritional status by providing information not available through other means and by forming the basis for a logical rationale for interventions. Further, this set of tools can be used to define more rigorously the nutrient requirements of individuals and population groups and, thus, their dietary recommendations.

Considerable progress has been made in associating gene variants with particular conditions, understanding how these variants alter responses to food, and how to use food to elicit desired gene responses. There is no doubt that much research remains to be carried out. Studies with greater numbers of healthy individuals stratified by genotype, age, and sex with carefully controlled dietary and other lifestyle interventions will certainly provide additional valuable information. It is our collective opinion, however, that there is a solid foundation upon which to screen for gene variants and adjust recommendations for lifestyle choices based upon the information currently available. We cannot stress enough the need for practitioners to use the scientific literature as their primary source of information and to regularly adjust their recommendations in line with new findings as they emerge in this rapidly moving field.

Nutrigenomics has already come a long way—far enough for dietetics professionals to realize that the future of nutrition will be interwoven with genetic information. The time has come for us to embrace and absorb the new and exciting opportunities that nutrigenomics provides. A part of this learning will be the vigilance and questioning, identifying and understanding the sound and substantial research that already exists, while being on the lookout for new nutrigenomic research or being part of such collaborations that initiate research. As nutrition professionals, we need to position ourselves as the respected, credible nutrition professionals that are best able to translate and communicate the latest developments in nutrigenomics to the public. This includes investigating the companies and laboratories that offer nutrigenetic testing, asking the difficult questions alluded to in this article, and finding partners that we can trust as we bring nutrigenomics into our practices. Be constantly aware of the ethical, legal and social issues that will arise and seek answers from credible sources. By sitting on the sidelines and waiting for others to pursue these lines of questioning, we will likely miss out on a unique opportunity to join in the new era of nutrition. The future is now.

References


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About the authors:

Ruth DeBusk, PhD, RD a former university genetics professor in private practice combines genetics and nutrition. She is a founding member of and a current advisor to NCC and the author of ADA’s Genetics: The Nutrition Connection and the recently published It’s Not Just Your Genes! co-authored with Yael Joffe.

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Complementary Nutrition Meetings Review:

Laura W. Lagano, MS, RD

In addition to National Nutrition Month, March also seems to be Complementary and Alternative Medicine, or CAM, Month. Complementary & Natural Healthcare Expo, also known as CAM Expo, took place on March 3rd to 5th in Manhattan; Integrative Nutrition Therapy Conference for Dietitians, Nutritionists, and Students was presented on March 16th in Brooklyn; and Nutracon preceded Natural Products Expo West and SupplyExpo on March 22nd to 24th in Anaheim.

For the first time, Nutrition in Complementary Care was a collaborating partner with CAM Expo (www.camexpo.com) and featured an exhibit booth in a prime location outside the keynote address hall. Many thanks to NCC members Nancy Case, Mary Gocke, Danny Jaghab, Mary Beth McCue, Sylvia Pisarski Onusic, Regina Ragone, and Kathie Swift for staffing the booth. Feedback from attendees including naturopaths, holistic nurses, CAM-oriented physicians, and homeopaths was positive and encouraging.

NCC member MaryBeth Augustine, who is an integrative medical nutritionist at Beth Israel's Continuum Center for Health & Healing in Manhattan, provided a cooking demonstration with culinary nutritionist Stephanie Sacks titled “Against the Grain: The Use of Gluten-Free Diets in Autoimmune Disorders.” Augustine believes that celiac disease is just the tip of the iceberg of gluten intolerance. “Far more ominous, hidden, and undetectable are the underwater rocks — the multi-system immune involvement. There is an abundance of scientific literature on autoimmune conditions that are associated with celiac disease, characterized by elevated gluten antibodies or villous atrophy or improved with the use of a gluten-free diet. Dietitians are ideal clinicians to identify gluten intolerance based on medical and diet history and a probing assessment of a patient’s symptomatic complaints, especially when autoimmune disease is present or suspect.

Though this was the only presentation featuring a registered dietitian, NCC had a good presence at the meeting with distribution of the Winter 2006 newsletter and the new, member benefit bookmark. (To request a copy of the bookmark contact Kathy Bernard at nccadmin@optonline.net.)

Mark Hyman, MD, author of the current bestseller UltraMetabolism, noted that “Alternative medicine is the medicine of the past being brought into the present and functional medicine is the medicine of the future being brought into the present.” According to NCC member Kathie Swift, who works with Hyman at Hyman Integrative Therapies, “Nutritionists and doctors must partner together to help patients by using a functional approach and nutrition assessment tools to unravel the origins of disease to help restore patients’ health. Something as simple as a vitamin D test, celiac panel, or serum homocysteine can no longer be overlooked because of cost, poor insurance reimbursement, or practitioner ignorance. Medical nutrition therapy is at a functional crossroad and the dietitian’s clinical skills must be highly seasoned.”

Brooklyn College held its First Annual Integrative Nutrition Therapy Conference for Dietitians, Nutritionists, and Students, (http://academic.brooklyn.cuny.edu/health/rschnoll/conference/program.htm) featuring NCC members Roseanne Schnoll and registered dietitians Carl Germano and Linda Lizotte among others. Topics covered nutrition for the immuno-compromised patient; diet and learning disorders; integrating complementary nutrition therapies into a successful practice; and nutritional approaches to pain management. “Nutritional factors such as food additives, refined sugars, food sensitivities/allergies, and fatty acid deficiencies have all been linked to ADHD,” said Schnoll. Though ADHD typically necessitates multiple treatment modalities, Schnoll believes that it’s judicious to first investigate nutritional and diet therapies before placing children on a regimen of potentially harmful psychostimulant medications. NCC also had presence at this meeting with distribution of the Winter 2006 newsletter and the member benefit bookmark.

Nutracon (www.nutraconferencce.com), which draws varied attendees, such as health professionals, food scientists, ethnobotanists, and food and supplement industry executives, celebrated the meeting’s 8th anniversary. Preceding Natural Products Expo West, “the largest gathering of the natural, organic, and healthy product industry,” Nutracon provides a top-notch networking opportunity for anyone interested in the most current advances in nutrition and product development. According to Todd Runestad, science editor of Functional Foods Nutraceuticals, “Over 15,000 new products or ingredients are introduced into the natural products market every year.” American BioSciences, Inc. earned the NutraAward for best new product -- a dietary supplement called Ave™. The supplement contains Avemar™ a fermented wheat germ standardized to methoxy-substituted benzoquinones (DMBQ). Numerous peer-reviewed, clinical studies demonstrate that Ave supports immune system modulation and the regulation of cell metabolism, positively impacting the processes of cell differentiation and repair.
Complementary Nutritional Meetings Review

NCC’s incoming chair Doug Kalman who is the Director of Nutrition and Endocrinology Research at Miami Research Associates presented on “Designing Clinical Trials for Maximum Return.” Kalman stated, “As time marches on, the government, consumers, and health professionals want to have confidence in the claims and product labels on natural products marketed for health.” He believes that these substantiation studies are needed from regulatory and legal perspectives as part of a safety net. All dietary supplement companies should work true R&D into their yearly budgets,” according to Kalman.

Upcoming Complementary Nutrition Meetings

Managing Biotransformations: The Metabolic, Genomic and Detoxification Balance Points
http://www.functionalmedicine.org/eduprog/symp_next.asp
April 19-22; Tampa, FL

Balancing One’s Health: Moving from Education to Motivation
610-436-6931
April 21-22; West Chester, PA

Neurochemical & Hormonal Consequences of the Modern Lifestyle
seminars@neuroscienceinc.com
April 29; New York, NY

Nutrition and Alzheimer’s Disease/Cognitive Decline
http://www.crha.rush.edu/IANA2006Symposium
May 1-2; Chicago, IL

Nutrition and Health: State of the Science Clinical Applications
http://columbiacme.org
May 1-3; New York, NY

SupplySide East
http://suppliesideshow.com/east
May 1-3; Secaucus, NJ

All Things Organic
www.organicexpo.com
May 5-6; Chicago, IL

Functional Foods and Nutraceuticals for Health Care Cost Reductions
May 12; Toronto, Canada

NIH State-of-the-Science Conference on Multivitamin/Mineral Supplements and Chronic Disease Prevention
http://www.consensus.nih.gov
May 15-17; Bethesda, MD

North American Research Conference on Complementary & Integrative Medicine
http://www.imconsortium-conference2006.com
May 24-27; Edmonton, Canada

Medicines from the Earth
www.botanicalmedicine.org
June 2-5; Black Mountain, NC

American Holistic Medical Association
www.holisticmedicine.org
June 7-10; St. Paul, MN

Current Concepts in Complementary and Alternative Medicine: Evidence-Based Medicine
www.hopkinscme.net
June 8-9; Baltimore, MD

Food as Medicine
http://www.cmmbm.org/brochure/FAM06-brochure.pdf
June 10-16; Baltimore, MD

Functional and Specialty Beverages: Market, Regulations, Processing, Formulation and Health Benefits
http://www.worldnutra.com/2006/orlando/Orlando_Short_Course.pdf
June 23-24; Orlando, FL

International Research Conference on Food, Nutrition and Cancer
airc@pearsonplanners.com
July 13-14; Washington, DC

National Nutritional Foods Association Convention & Trade Show
www.nnfa.org
July 14-16; Las Vegas, NV

If you would like to report on a meeting or list an upcoming meeting that has relevance to NCC please contact Publications Chair Laura Lagano at lwlagano@optonline.net.
The Individualization of Nutrition Assessment, Treatment, and Prevention in the Post-Genomic Era

Kipp Ellsworth, MS, RD, CSP, LD, CNSD

The completion of the Human Genome Project (HGP) in 2003 marked a seminal event in the annals of scientific achievement. The HGP afforded scientists universal access to the entire genetic sequence and enabled the production of gene maps of the human genome, highlighting inherited genetic variability. During his testimony before the US House of Representative’s Subcommittee on Health in 2003, Dr. Francis Collins evoked a vision for the future of genomics research, developed by the US National Human Genome Research Institute.

The vision included the opportunity to understand the role of genetic factors in health and disease, and to apply that understanding to prevention, diagnosis, and treatment. In particular, genomics-based approaches could allow more precise prediction of disease susceptibility and drug response, earlier detection of disease, and the development of novel therapeutic approaches.

From the Pre-Genomic to the Post-Genomic Era

Making the transition from the pre-genomic to the post-genomic era may be characterized as building the framework to make the results of genomics research applicable to individuals. Pathways from genomic information to improved human health are being forged via the cataloguing of as many of the genetic variations within the human genome as possible. Naturally occurring genetic variations known as single nucleotide polymorphisms (SNPs) are being stored in vast databases for access by researchers in their efforts to explore the potential relationship between disease and genomic variation. Recent advances in technology, coupled with the unique ability of these normal genetic variations to facilitate gene identifications, have led to a flurry of SNP discovery and detection. This exploration is being conducted utilizing bioinformatics technology, which consists of mathematical tools to extract applicable biomedical information from databases produced by highly efficient biological techniques such as gene and protein expression analysis. In this capacity, genomics has been successfully integrated into the more applied discipline of biomedical research. Most interestingly, the pathway from genomics to human health has also focused on how genomic variation affects not only drug metabolism and response, but also nutritional metabolism and response.

The first clinical beneficiary of the HGP and its cataloguing of polymorphisms was the field of pharmacogenomics and its concentration on inherited variability in drug disposition and metabolism. Polymorphisms can cause alterations in drug effect by means of variation in drug receptors and transporters, cell signaling, and metabolism, resulting in disparity in drug efficacy, dosing, and toxicity profile. Pharmacogenomics has capitalized on the bioinformatics revolution and evolved beyond simple studies of variability to detailed research in all aspects of drug behavior such as absorption, distribution, metabolism, excretion, and receptor-target affinity. Pharmacogenomics offers the potential for individualized drug therapy based on patient genotype and the promise of improved clinical medicine via expedited dose adjustment and decreased patient morbidity and mortality.

Although pharmacology was the first discipline to utilize bioinformatics technology to screen for SNPs quickly and affordably, medical nutrition has been following closely. Nutrigenomics, which studies the interaction among genetic variations, dietary components, and the health and disease potential of a person, offers the promise of preventing or delaying the onset of disease and optimizing human health through individualized nutrition.

Bioinformatics is utilized to identify polymorphisms associated with nutrition for potential application as biomarkers to aid in the individualized assessment of disease risk, as well as nutritional status and requirements. The use of biomarkers as an indicator of drug or nutrient metabolism is expanding beyond disorders determined by a single gene (monogenic) to those resulting from the combined action of more than one gene (polygenic). This article reviews the interrelationship between heterogeneity in drug and nutritional metabolism, and both monogenic and polygenic variation.

Clinical Variance and Monogenic Disorders

The emergence of pharmacogenomics was propelled by innovations in bioinformatics analysis as well as an enhanced understanding of all aspects of drug behavior. Interindividual variability in drug response was increasingly observed to be correlated with single gene polymorphisms, causing altered gene product function in comparison to the benchmark gene (wild-type DNA). Much of the variability in drug response has been linked to polymorphisms in genes for the cytochrome P450 (CYP) family of enzymes responsible for the metabolism of the majority of drugs entering the animal body. Polymorphisms affecting — CYP function and expression can influence drug response; most notably via mutations that inactivate a member of the CYP, causing an absence of effective gene product, and consequently poor metabolism of the enzyme’s substrate. In particular, the literature frequently cites polymorphisms in the drug metabolizing enzyme CYP 2D6 as being paradigmatic for a wide range of polymorphisms affecting drug response.

CYP 2D6 is responsible for the hydroxylation of debrisoquine, formerly used in the treatment of essential hypertension, to form 4-hydroxydebrisoquine. Studies identified certain patients as either extensive or poor debrisoquine metabolizers, with the poor metabolizers unable to form the 4-hydroxy product and...
experiencing significant hypotension. In addition to poor and extensive metabolizers, a group with intermediate metabolic characteristics (falling between the poor and extensive categories), and a group of ultra-rapid metabolizers was observed, thus resulting in four clinically distinct manifestations of genetically-based CYP 2D6 hydroxylase trait (phenotypes). Not only are poor metabolizers at risk for adverse reactions to debrisoquine, but they are also at risk for insufficient metabolism of a wide variety of drug substrates upon which CYP 2D6 acts. These include greater than 50 major drugs; most notably the anti-arrhythmic drugs sparteine and propafenone as well as the tricyclic antidepressant amitriptyline. In addition to poor metabolizers, CYP 2D6 polymorphisms that result in inactivation of enzyme activity may interfere with activation of the substrate medication. Codeine, which requires conversion to morphine for analgesia, is ineffective in patients with CYP 2D6 polymorphisms, thereby preventing its activation. The prevalence of inactivating CYP 2D6 polymorphisms in the population may explain the significant variation of effective codeine dose for pain relief.

Similar to variability in pharmacologic response, variability in nutritional metabolism has also been associated with single gene polymorphisms. Major inborn errors of amino acid metabolism are illustrative of the numerous clinical phenotypes associated with polymorphisms in a single gene. Equally paradigmatic as CYP 2D6 are polymorphisms in the gene for phenylalanine hydroxylase (PAH), an enzyme responsible for the conversion of phenylalanine to tyrosine, which are linked to abnormal levels of phenylalanine in the blood and urine characteristic of the disorder phenylketonuria (PKU). In fact, greater than 440 polymorphisms in the PAH gene have been documented. These polymorphisms underlie four distinct PKU phenotypes in the population based on phenylalanine levels at diagnosis and dietary tolerance of phenylalanine: classical PKU, moderate PKU, mild PKU, and mild hyper-phenylalaninemia. A subset analysis of PAH polymorphisms revealed three distinct groups of genetic sequences (genotypes) based on associated PAH enzyme activity: inactive enzyme with insignificant protein expression, moderate (10% to 70%) wild-type activity and protein expression, or significant (80% to 100%) enzyme activity and protein expression. Utilizing these data the researchers conducted PKU genotype-to-phenotype associations revealing that of seven genotypes of the first group, five were associated with classical PKU and two with moderate PKU; of seven genotypes of the second group, one had classical PKU, one had moderate PKU, and five had mild PKU; of five genotypes of the third group, two had mild PKU and three had mild hyperphenylalaninemia.

Making the genotype-to-phenotype transition has tremendous implications when attempting to adjust for variability in not only drug response, but also in nutritional metabolism. Even within the context of clinically normal heterozygotes possessing one wild-type allele, extreme circumstances may prompt adverse consequences in drug or nutrient metabolism as a result of partial defects in enzyme activity.

Clinical Variance and Polygenic Disorders

In contrast to the monogenic paradigms CYP 2D6 and PAH, the majority of genetic predispositions to disease and pharmacogenetic traits are polygenic and multifactorial. In multifactorial inheritance the influence of several genes is often overlaid by environmental (i.e. nutrition) factors so that the overall phenotype is highly variable interindividually, and within individuals across time. Risk factors for common multifactorial polygenic diseases such as cardiovascular disease (CVD), diabetes, obesity, hypertension, and cancer must take into account both genetic and environmental factors. Thus, research within the context of polygenic disease is focusing on the elucidation of biomarkers to help account for interindividual variability in dietary response.

Perhaps the most compelling research efforts to individualize drug therapy within the context of polygenic disease are being conducted in cancer pharmacogenomics. Combining drug-pathway analysis and studies assessing the effects of polymorphisms in drug targets and drug-metabolizing enzymes, clinical trials have demonstrated the predictive power of chemotherapy activity and response to drugs such as mercaptopurine, 5-fluorouracil, and cyclophosphamide. Utilizing polygenic pharmacogenomic strategies, it is hoped that prescreening cancer patients for well-characterized polymorphisms will enable the best-tolerated and most effective treatment strategies to be identified.

Paralleling pharmacogenomic studies, nutrigenomic studies are increasingly focusing on the statistical interaction between polymorphisms at multiple loci and dietary intake in determining the outcomes of multifactorial disorders. Understanding the biological impact of gene-nutrient interactions is providing a key insight into the pathogenesis and progression of diet-related polygenic diseases such as cancer and CVD. Research examining gene-diet interactions in CVD indicates the potential modification of CVD risk via the effect of genetic variation on the lipid response to dietary intervention. Several genes whose products affect lipoprotein metabolism, such as apolipoproteins, enzymes, and receptors, are providing evidence to support the role of personalized nutrition in CVD prevention and treatment. For example, polymorphisms in the lipoprotein lipase (LPL) gene have been shown to influence the response to dietary therapy. Researchers evaluated the effect of a high saturated fat diet and a high polyunsaturated fat diet on cholesterol response in a double crossover trial. They found that variation in the genes for LPL and cholesterol ester transfer protein predicted total cholesterol response, independent of measures of dietary compliance. In addition, researchers seeking to identify genetic factors related to individual difference in lipid responses to intensified treatment in Type 2 diabetes found that LPL genetic variation, independent of therapeutic intervention, affected changes in HDL-cholesterol and was associated with the frequency of coronary heart
disease. By continuing to investigate the effects of polymorphisms in multiple genes rather than in single genes, researchers will enhance our ability to develop effective nutrient-based preventive and therapeutic strategies to combat diet-related polygenic disorders.

Future Directions

The successful utilization of nutrigenomics in providing individualized recommendations for common multifactorial disorders will require the convergence of different disciplines working on large population studies designed to investigate gene-environment interactions. For nutrition professionals, an understanding of the relationship between clinical heterogeneity and genetic variation constitutes a necessary prelude to adoption of a nutritional systems biology approach to assessment and treatment. The new discipline of metabolomics is focusing on the comprehensive profiling of metabolites such as sugars, fats, RNA, and proteins in the cells of organisms at specific times and under specific conditions. The analytic processes characteristic of metabolomics, such as spectroscopy and chromatography, allow scientists to link physiologic effects and drug reactions to a greater understanding of health and human metabolism. The ability to clinically evaluate disease utilizing metabolite profiling strategies, in concert with nutrigenomics, will have major implications for prognostic evaluation and the monitoring of treatments.

Take Home Message

The post-genomic era has highlighted the tremendous therapeutic potential of applying genetic data to the customization of pharmacologic and nutritional interventions. The challenge for nutrition professionals in the post-genomic era is two-fold. First, assessments must transcend the traditional health care paradigm that focuses solely on the modification of the environment to improve clinical outcome. Genetic variation must be recognized as an increasingly valuable marker by which to assess risk and customize intervention. Second, the nutrition professional must evolve beyond the one-dimensional single gene, single dietary factor paradigm that pervades traditional health care. Health interventions in the post-genomic era warrant a transdisciplinary approach based on an appreciation of an individual's genetically-based pathophysiology and its potential interactions with dietary factors. By embracing the tools of genomics nutrition professionals will not only benefit more directly from the insights of related fields, but also continue to evolve to meet the demands of their clients in the era of postgenomic customization.

Kipp Ellsworth is a clinical nutritionist at Children's Healthcare of Atlanta at Egleston providing oversight to the implementation of nutrition support regimens in gastroenterology, pulmonology, cystic fibrosis, and pediatrics. His interests are in nutrigenomics, particularly the genetics of the inflammatory response and potential nutrigenomic applications to pediatric inflammatory bowel disease.

References

Learning Objectives for the Nutrigenomics Article

After reading the CPE article the nutrition professional will be able to:

1. Define and distinguish between nutrigenomics and nutrigenetics.
2. State the relevance of nutrigenomics to dietetic practice.
3. List career paths and options for the dietetic practitioner interested in pursuing work in the emerging field of nutritional genomics.
4. Outline the genetic screening process for diet-related gene variants.
5. Recite questions that the individual seeking genetic screening should ask prior to choosing a screening tool.
6. Name one gene variant (SNP) that has a diet related component.
7. Discuss diet related modification(s) or lifestyle intervention(s) that should be employed for a specified SNP(s).
It’s Not Just Your Genes

Ruth DeBusk
Yael Joffe

BKDR, Inc. Publishing
San Diego, CA: 1-619-223-7775
250 pp; paperback: $15.95:
ISBN: 0977636305

It’s Not Just Your Genes! is intended for lay persons interested in nutrigenomics and its personal application; however, it is a great resource for the nutrition practitioner as well.

If BB-BB yields brown eyes and Bb-Bb yields brown eyes or blue eyes is all that is recalled from the genetics lecture of freshman biology 101, then It’s Not Just Your Genes! is a must read. DeBusk and Joffe explain the emerging complex science of genomics in understandable language complete with graphics and illustrations. For the nutrigenomics naïve nutrition practitioner It’s Not Just Your Genes! is an excellent primer. A subsequent must read is DeBusk’s Genetics, The Nutrition Connection.

The book is systematically organized. The science of genetics and nutrigenomics is introduced. Subsequent chapters examine a specific chronic diseases (cardiovascular, cancer, diabetes mellitus, osteoporosis, and obesity), the gene variant(s) associated with the disease, and nutrition intervention(s) likely to influence gene expression. Within each chapter there is a summary table outlining the gene variant, gene name, gene action, and influence of lifestyle factors. Concomitantly, throughout the book, there are tables of foods and nutrients and sample menus and recipes to facilitate ingestion and consumption of select foods/nutrients. The appendices and resources and notes are helpful and informative both for the lay person and the nutrition professional.

DeBusk is pioneer in the field of nutrition and genetics. With 40+ years in the field of nutrition and genetics she has authored numerous papers and lectured extensively in the classroom of university students and professional practitioners. Joffe serves as the Director of Diet and Nutrition for Sciona Inc., a provider of nutrigenomics testing services. Concurrently, she is pursuing doctoral work on the genetics of obesity.

Reviewed by Katherine Stephens-Bogard MS RD CDE CPE coordinator for the NCC newsletter. Katherine specializes in diabetes and endocrine metabolic disorders at The Washington Hospital in southwestern Pennsylvania. Contact Katherine at ksbrlb@ovis.net or kstephensbogard@washingtonhospital.org or 724-250-6298.
CONGRATULATIONS

Thank you for voting for our 2006-2007 NCC Leadership
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News from ADA

The Hot Topics on DNA and Diet is up on the ADA Web site - see http://www.eatright.org/cps/rde/xchg/ada/hs.xsl/nutrition_8177_ENU_HTML.htm.

Read a discussion of the claim that choosing foods appropriate to our genetic makeup can minimize our risk of disease and maximize the ability to perform at our optimal genetic potential.

Hot Topics was designed to respond to member’s request for current scientific-based information on popular consumer and media driven nutrition concerns. The Association Positions Committee (APC), the committee that oversees the position development process, along with ADA staff is overseeing the Hot Topics process.
**The Effect of Hot Water Infusions of Broccoli Sprouts on Biomarkers of Carcinogen Metabolism**

Kensler T, Chen J, Egner P, et al.


There is a very high incidence of hepatocellular carcinoma in the Qidong region of the People's Republic of China. In some rural townships this disease is the cause of death for up to 10% of adults. The putative explanation for the unusual prevalence of this form of cancer is the presence of aflatoxins (any of several carcinogenic mycotoxins that are produced especially in stored agricultural crops [as peanuts] by molds [as Aspergillus flavus]) in the diet, in conjunction with chronic infection with the hepatitis B virus. Public health experts are therefore attempting to reduce the incidence of this disease through vaccination programs against the hepatitis virus, as well as reducing exposure to aflatoxin. It is too soon to evaluate the effectiveness of the vaccination program in main land China. However, a universal vaccination program in Taiwan has resulted in lower rates of hepatocellular carcinoma in children.

Since liver cancer is so pervasive in certain parts of the world, and since complete eradication of mold-generated aflatoxins in foods is not possible, researchers have been investigating a series of chemopreventive strategies to reduce the likelihood of cancer as an outcome to incidental exposure to aflatoxins. The first such trial utilized chlorophyllin to block carcinogen bioavailability, by forming molecular complexes with aflatoxin in the gastrointestinal tract. This intervention is safe and inexpensive. However, the necessity of taking the chlorophyllin tablets 3 times per day over long periods of time could result in poor compliance. In the second trial, oltipraz (Oltipraz 5-[2-pyrazinyl]-4-methyl-1,2,3-thione) is currently undergoing phase I trials in the United States. Originally developed as an antischistosomal [parasite killing] agent, it was found to protect against chemically induced carcinogens in the lung, stomach, colon, and urinary bladder in animals. It was administered once daily and resulted in enhanced metabolic detoxification of aflatoxin. In animal models, it has been found that small molecules can be administered as little as once per week to induce protective phase 2 enzyme pathways. However, oltipraz has several shortcomings as a chemopreventive agent including cost, availability and adverse side effects. Therefore, the authors continued their search for a feasible method of stimulating aflatoxin detoxification.

Epidemiological studies suggest that ingesting large quantities of fruits and vegetables in general, and cruciferous vegetables (broccoli, cabbage, kale and Brussels sprouts - members of the family Cruciferae a.k.a. Brassicaccae) in particular, results in a reduced risk of gastrointestinal and other cancers. In laboratory research with mammalian cells, researchers have identified phytochemicals, called glucosinolates, in broccoli that induce detoxification enzymes and strengthen antioxidant activity. Sulforaphane, (an isothiocyanate molecule) is primarily responsible for this inducer activity. Glucoraphanin is converted into sulforaphane by the enzyme myrosinase, which is released when food is chewed, or by enteric bacteria in the human gastrointestinal tract. Sulforaphane and glutathione are conjugated by liver enzymes (GST’s) to form a series of metabolites, collectively called dithiocarbamates, which are excreted in the urine. The predominant end product of this pathway is mercapturic acid.

Glucosinolates, the precursors to isothiocyanates, are found in many edible plants of the Cruciferae and other plant families. However, young broccoli plants are an extremely rich source of glucosinolates, containing 20-50 times the amount found in mature broccoli plants. Glucoraphanin, the precursor to sulforaphane, is the most abundant glucosinolate in broccoli seeds and 3-day-old broccoli plants. In rodents, dietary broccoli sprouts have been shown to afford protection against chemically induced tumors, through induction of the phase 2 response by glucosinolates.

This randomized clinical trial evaluated the efficacy of a broccoli sprout infusion to diminish urinary levels of 2 biomarkers associated with environmental carcinogenesis. The primary end point is aflatoxin-N7-guanine. Elevated levels of this aflatoxin-DNA adduct excretion product are associated with an increased risk of liver cancer. The secondary endpoint is r-1,r-2,3,c-4-tetrahydroy-1,2,3,4-tetrahydropheanthrene (trans, anti-PhET). This molecule reflects exposure to, and biotransformation of polycyclic aromatic hydrocarbons (PAH), which are well-documented human carcinogens.
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Study participants were recruited from the rural farming community of He Zuo Township, Qidong, Jiangsu Province, People’s Republic of China, and screened at the He Zuo Township hospital. In this trial, two hundred adults between the ages of 25 and 65 were enrolled and randomized into 2 intervention arms. Participants were in generally good health without major chronic illnesses. Hepatitis B surface antigen positive individuals with normal liver function were included in the trial. Researchers from the Qidong Liver Cancer Institute and Johns Hopkins University conducted the study.

Investigators prepared the intervention beverage by sprouting 40 kg of broccoli seeds (Caudill Seed Co., Louisville, KY) for 3 days and producing a hot water extract from the resulting 200 kg of sprouts. The intervention beverage was bottled in 125 mL aliquots (being an equal fractional part) and immediately frozen. After rinsing the sprouts with cold water, the second and third boiling water extractions were discarded. The fourth hot water infusion was used as the placebo beverage. Both the placebo and infusions were analyzed by several methods to confirm that the placebo contained at least 100-fold lower levels of glucoraphanin than the intervention beverage.

Participants were given a comprehensive list of glucosinolate-containing foods, and asked to avoid these foods for a 3-day run-in period, and during the course of the 2-week trial. During the run-in period study investigators visited participants in their homes at dinnertime to observe the composition of meals. During the trial, the study investigators distributed the intervention beverages (125 mL doses, each containing 400 micromol glucoraphanin) between 5 and 6 p.m. at the homes of local doctors.

Only 1 person dropped out of the study, and compliance with the study protocol was outstanding. Urinary dithiocarbamate levels did not increase significantly in the placebo group. In those drinking the broccoli sprout beverage, dithiocarbamate levels increased dramatically (P<0.001) vs. the run-in period.

The outcome of this trial was negative with respect to modulating levels of the primary and secondary urinary biomarkers (aflatoxin-N7-guanine and trans, anti-PheT). On day 10 there was a statistically insignificant 7% decrease in urinary excretion of aflatoxin-N7-guanine in the treatment group vs. the placebo group. In day 9 urine samples, there was a statistically insignificant 28% reduction in urinary excretion of trans, anti-PheT compared to the placebo group. However, when certain factors relating to biochemical individuality are taken into consideration, and the data is analyzed from a different perspective, a completely different picture emerges.

The hot water extract was selected for the study due to several considerations, including the logistical and hygienic challenges of providing a consistent source of fresh sprouts in a rural, undeveloped region. However, the authors write that “[a] major disadvantage of using hot water extracts of broccoli sprouts as opposed to intact broccoli sprouts lies in the capacity for hydrolysis of glucoraphanin to sulforaphane. The plant enzyme catalyzing this hydrolysis, myrosinase, becomes inactivated by boiling. Glucosinolates per se are inert as phase 2 enzyme inducers and must be hydrolyzed to generate the active isothiocyanates.” Therefore, the bioavailability of sulforaphane is dependent on the capacity of each individual to convert glucosinolates into isothiocyanates via enteric bacteria. Researchers discovered that “although sulforaphane bioavailability was reasonably consistent between doses within an individual, there was 3-fold greater variabil-

When the study data was analyzed after controlling for the bioavailability of sulforaphane in each individual, the intervention showed positive results. There was a significant inverse association between dithiocarbamate and aflatoxin-N7-guanine concentrations in the group receiving the broccoli sprout beverage (P<0.002). This inverse association was more robust when a 1-day lag was brought into the dithiocarbamate and aflatoxin measurements, suggesting, “that yesterday’s pharmacodynamic action of sprouts principally affects today’s carcinogen biomarker excretion.” There was also a highly significant inverse association between log [trans, anti-PheT] and log [dithiocarbamate] in day-9 urine samples from the broccoli sprout infusion group (P<0.0001). There was no association for these parameters in the placebo group.

This randomized clinical trial demonstrates that consumption of a broccoli sprout infusion can modulate excretion of 2 independent markers of carcinogen metabolism. The results “suggest that sulforaphane was exerting a pharmacodynamic action in at least a subset of the participants.” Methods need to be developed to provide a consistent yield and bioavailability of sulforaphane from infusions of broccoli sprouts. "Nonetheless, these results provide an expectation that food-derived chemopreventive agents can be administered in defined, rational, and practical ways to favorably modulate the disposition of unavoidable exposures to environmental carcinogens.”

-Cathleen Rapp, ND
CPE Questions

1. Nutritional genomics (nutrigenomics) is expected to have relevance for which of the following dietetic focus areas:
   A. Clinical nutrition
   B. Food science research
   C. Nutrition research
   D. Food development
   E. All of the above

2. A gene is a sequence of DNA nucleotides that contains within it the instructions for synthesizing a protein.
   A. True  B. False

3. A relatively new term used to describe the wide variety of components within food (or dietary supplements) that can interact with the genetic information to affect function is:
   A. Nutrients
   B. Phytochemicals/phytonutrients
   C. Bioactive food components, sometimes shortened to "bioactives"
   D. Non-nutritive components

4. An example of a nutrigenetic application is an increased requirement for folate in an individual with the MTHFR 677C>T gene variation.
   A. True  B. False

5. An example of a nutrigenomics application is increasing an individual’s intake of omega-3s in order to decrease expression of the pro-inflammatory genes.
   A. True  B. False

6. Which type of testing is the most relevant to nutrigenomics?
   A. Detection of human mutations that definitively cause disease
   B. Detection of human gene variations that are incapable by themselves of causing disease but confer increased susceptibility to disease
   C. Testing of genetically modified food
   D. Detection of genes in plants

7. A SNP is a:
   A. Somewhat neutral phenotype
   B. Cut in a strand of DNA
   C. Single nucleotide polymorphism
   D. Small neutrophil piece

8. In order for a SNP to have relevance to nutrigenomics applications, it must:
   A. Alter function in a way that’s readily measurable
   B. Have a clear association with a condition/physiological outcome
   C. Have a clear association with a measurable diet-gene interaction
   D. Be associated with food and nutrition recommendations that can positively affect the influence of the SNP on physiological outcomes
   E. Be evidence based, i.e. supported by a significant amount of peer-reviewed literature concerning the SNP and its effects
   E. All of the above

9. Among the questions to ask when considering nutrigenomics testing are:
   A. How do you protect an individual’s privacy?
   B. If the consumer has not consented to the use of their DNA sample for research purposes, is the sample destroyed once testing is completed?
   C. Which SNPs are included in your genetic testing panels?
   D. Which peer-reviewed studies substantiate the use of the SNPs in your test panels?
   E. All of the above

10. The most effective lifestyle approaches for improving dyslipidemia in someone with at least one copy of the E2 allele of the APOE gene is a diet that:
    A. Controls saturated fat and restricts total fat to 20% or less of energy
    B. Controls the intake of simple carbohydrates
    C. Includes oat bran and other soluble fibers
    D. Includes supplementation with omega-3 fatty acids
    E. Includes regular endurance (aerobic) exercise
    F. Allows for moderate intake of alcohol
    G. All of the above
    H. All except (A)
    I. All except (A and F)

11. Nutrigenomics is an appropriate career option for dietetics professionals.
    A. True  B. False

12. Which of the following represent career paths for dietetics professionals with competency in nutrigenomics?
    A. Member of a research team developing SNP-based genetic tests for early detection of susceptibility for hypertension
    B. Food scientist developing dietary supplements specifically designed to reduce disease risk identified by particular gene variants
    C. Educator working with retail food outlets to develop materials to help consumers make food purchasing decisions appropriate for their genotype
    D. Clinical trial coordinator involved with testing the strength of association between a SNP and a disease state
    E. All of the above

Answer Key


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