Position of the Academy of Nutrition and Dietetics: Nutritional Genomics

ABSTRACT

It is the position of the Academy of Nutrition and Dietetics that nutritional genomics provides insight into how diet and genotype interactions affect phenotype. The practical application of nutritional genomics for complex chronic disease is an emerging science and the use of nutrigenetic testing to provide dietary advice is not ready for routine dietetics practice. Registered dietitian nutritionists need basic competency in genetics as a foundation for understanding nutritional genomics; proficiency requires advanced knowledge and skills. Unlike single-gene defects in which a mutation in a single gene results in a specific disorder, most chronic diseases, such as cardiovascular disease, diabetes, and cancer are multigenetic and multifactorial and therefore genetic mutations are only partially predictive of disease risk. Family history, biochemical parameters, and the presence of risk factors in individuals are relevant tools for personalizing dietary interventions. Direct-to-consumer genetic testing is not closely regulated in the United States and may not be accompanied by access to health care practitioners. Applying nutritional genomics in clinical practice through the use of genetic testing requires that registered dietitian nutritionists understand, interpret, and communicate complex test results in which the actual risk of developing a disease may not be known. The practical application of nutritional genomics in dietetics practice will require an evidence-based approach to validate that personalized recommendations result in health benefits to individuals and do not cause harm.
J Acad Nutr Diet. 2014;114:299-312.

POSITION STATEMENT

It is the position of the Academy of Nutrition and Dietetics that nutritional genomics provides insight into how diet and genotype interactions affect phenotype. The practical application of nutritional genomics for complex chronic disease is an emerging science and the use of nutrigenetic testing to provide dietary advice is not ready for routine dietetics practice. Registered dietitian nutritionists need basic competency in genetics as a foundation for understanding nutritional genomics; proficiency requires advanced knowledge and skills.

THE SCIENCE OF GENETICS AND genomics is moving at an accelerated pace. New technologies and scientific discoveries are deepening our understanding of how nutrients and dietary patterns affect health maintenance and disease development. Advances in epigenetics and the influence of the microbiome on health and disease also are contributing to the understanding of nutrition and health. Many omic approaches—transcriptomics, proteomics, and metabolomics—will help us understand nutrient–genome interactions. Genotyping alone will not be sufficient to personalize diet for improved health.[1] Understanding and manipulating how diet affects the phenotype of an individual will require technologies that can reveal the processes of what happens from the genetic blueprint through transcription and synthesis of proteins to identification of metabolites that will tell us what has happened, both abnormal and normal. Whereas new scientific discoveries and technologies continually inform the science of nutritional genomics, translating these scientific discoveries into practical clinical application requires obtaining the same rigorous evidence that is the backbone of dietetics practice.

2212-2672/$36.00
http://dx.doi.org/10.1016/j.jand.2013.12.001

SEQUENCING THE HUMAN GENOME

The first draft of the human genome was published in 2001 through an international effort called the Human Genome Project that took 20 years from inception to completion and cost $3 billion. This incredible accomplishment was a mere 150 years after Mendel manipulated the colors of peas leading to his discovery of autosomal recessive inheritance, 100 years after chromosomes were identified as bearing inherited traits, 50 years after Watson and Crick described the molecular structure of genetic material as the double helix, and 30 years after the first DNA sequencing technology was invented. The full sequence of the human genome was completed and published in 2003.[2] Perhaps the most startling discovery was that the number of human genes was estimated to be significantly fewer than early estimates. Since the completion of the Human Genome Project, hundreds of genomes have been sequenced from the tiniest bacteria to the largest mammal.[3] Technological advances have dramatically dropped the cost of sequencing a human genome from $95 million in 2001 to <$6,000 in 2013.[4] However, these costs do not reflect the costs associated with the development of bioinformatics, computational tools, equipment, and the analysis and interpretation of the data.[5] As the time and cost to sequence a human genome continues to drop, the expectation that it will become an integrated part of medical practice becomes more of a reality. However, translating whole genome sequencing into therapies that will benefit an individual will require strategies to handle large amounts of biological and medical data and the ability to identify significant and clinically meaningful results.[6]

GENETICS

Genes contain all of the biological information needed to build and maintain a living organism (see Figure 1). Genes are responsible for protein formation and, ultimately, metabolic function. Genes are turned on and off in response to metabolic signals that the nucleus receives from internal factors, such as hormones and enzymes, and external/environmental factors, such as diet.

Genes vary in size from a few hundred DNA bases to >2 million bases. Human beings have between 20,000

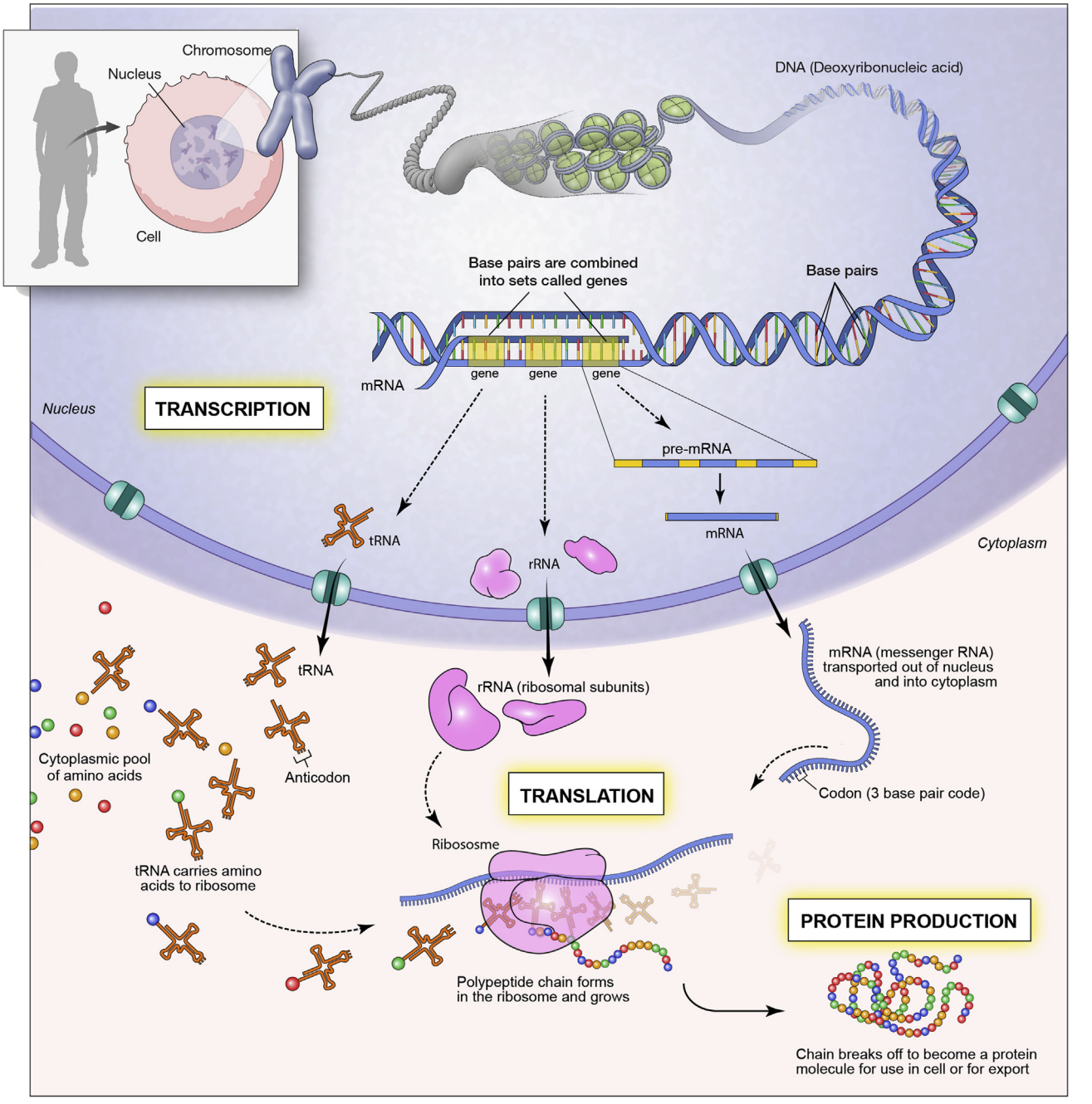

Figure 1. Within the nucleus of cells throughout our body are 23 pairs of chromosomes; within each chromosome is the genetic material organized into sequences known as genes. During the processes of transcription and translation, proteins are formed. In transcription, the information stored in a gene's DNA is transferred to RNA in the cell nucleus. Messenger RNA (mRNA) carries the message from the DNA out of the nucleus into the cytoplasm. In translation, mRNA interacts with ribosomes to read the sequence of mRNA bases. Each sequence of three bases, called a codon, usually codes for one particular amino acid. Each amino acid is brought to the ribosome by transfer RNA (tRNA). These tRNAs are specific for the particular amino acid they carry and recognize the codons along the mRNA.