Role of Nutrigenetics and Nutrigenomics in Precision Nutrition

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INTRODUCTION

Nutrigenetics deals with the genetic variations within a gene in a population group that affects nutrient metabolism. In contrast, the expression of genes influenced by bioactive compounds is referred to as nutrigenomics. Adaptation to diverse nutrition conditions resulted in the human evolution of nutrigenetics. Changes (polymorphism) often occur among individuals or populations due to two or more variant forms of a specific DNA sequence or gene. The most common type of polymorphism involves variation at a single nucleotide and is referred to as single-nucleotide polymorphism or SNP. These genetic variations cause roadblocks in metabolism in some population groups, whereas others remain unaffected. For example, Individuals with SNP rs762551 in CYP1A2 metabolize coffee differently and can have beneficial or harmful cardiovascular effects. Vitamin E intake by people with SNP rs4680 (met/met) in catecholamine methyl transferase (COMT) can be protective against cardiovascular and colon cancer. The presence of rs12325817 SNP in phosphatidylethanolamine methyl transferase (PEMT) limits endogenous production of phosphatidylcholine and imposes a risk of organ dysfunction in women and elderly populations. The C677T polymorphism in methylene tetrahydrofolate reductase (MTHFR) affects cellular methylation processes and results in the accumulation of homocysteine, causing hypertension. Lactose intolerance results from polymorphisms (SNPs) in the MCM6 gene. MCM6 lies upstream of the lactase gene and contains a regulatory region allowing lactase expression. Two sites of variation, rs4988235 and rs182549, independently evolved, and a mutation from the more common "wild type" C allele to a T allele causes continued lactase expression into adulthood. Studies found genetic variation in the Sucrose Isomaltase gene is associated with predisposition to Inflammatory Bowel Syndrome, which is attributed to a common coding variant, 15Phe at SNP rs9290264. Polymorphisms near CYP2Rl (rs2209314, rs2762939) affect 25-OH-vitamin D concentrations. XRCC1 genotype polymorphisms could modulate a higher prostate cancer risk associated with a lower lycopene and vitamin E intake. On the other hand, nutrients can modulate gene expression through epigenetic processes via histone modification, DNA methylation, and miRNA expression. Green tea (ECGC), Soybean (genistein), and Tomatoes (lycopene) inhibit, whereas Turmeric (curcumin), Red grapes (resveratrol), and Cabbage (sulforaphane) stimulate DNA methylation. Similarly, Vit D, PUFAs, CoQ10, and lycopene modulate the expression of miRNAs. These processes affect gene expression and thereby influence health/disease outcomes. Information from nutrigenetics and/or nutrigenomic can help formulate precision nutrition to target specific population groups.