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Nutrigenomics and nutrigenetics: Special emphasis on optimization of human health and animal performance

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Abstract

Environmental factors, food's nutrients, and genetic makeup play an important role in phenotypic appearance of a trait via the principles of biological sciences. The nutritional genomics focuses on the interaction between bioactive food components and the genome, which includes nutrigenetics and nutrigenomics. The influence of nutrients on genes expression is called nutrigenomics, while the heterogeneous response of gene variants to dietary nutrients is called nutrigenetics. Nutrigenomics is providing the effects of ingested food's nutrients on gene expression and gene regulation, i.e., diet-gene interaction in order to identify the dietetic components having beneficial or detrimental health effects. It elucidates that how DNA and genetic code influence the need for specific nutrients and also within specific quantities are required for maintaining good health throughout life. It is helpful to determine the personalized diet that means individual nutritional requirements based on the genetic makeup of the person as well as clarifies some etiological perspectives of chronic diseases like type-2 diabetes, cancer, obesity and cardiovascular diseases (CVD) because of associations between diet and chronic diseases. Rearing of farmed animals is a vital component of global food production systems, its impact on the environment, human health, animal welfare, and biodiversity is being increasingly challenged. Developments in genetic and genomic technologies have had a key role in improving the productivity of farmed animals for decades. The goal of discussing these issues is to get a better understanding of basic biological issues and to apply their knowledge to practical problems such as medicine, and improvement of animal performance. Therefore, this review article is focus on the role of genes and the use of genomic techniques in human health, as well as animals' well-being and welfare.

Keywords: Food's Nutrients; Genetics; Nutrigenetics; Nutrigenomics; Gene expression; Human health; Animal performance

1 Introduction

Nutrition is the biochemical and physiological process by which an organism uses food to support its life. It provides organisms with nutrients, which can be metabolized to create energy. Nutrients are chemical compounds in food that are used by the body to function properly and maintain health. These nutrients are proteins, fats, carbohydrates, vitamins, and minerals. Failure to obtain sufficient nutrients causes malnutrition. Moreover, a nutrient is a substance used by an organism to survive, grow, and reproduce. Nutrients can be incorporated into cells for metabolic purposes or excreted by cells to create non-cellular structures, such as hair, scales, and feathers. Some nutrients can be metabolically converted to smaller molecules in the process of releasing energy, such as for carbohydrates, lipids, and proteins. Different types of organisms have different essential nutrients. Ascorbic acid (vitamin C) is essential,

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meaning it must be consumed in sufficient amounts, to humans and some other animal species, but some animals are able to synthesize it. Nutrients may be organic or inorganic: organic compounds include most compounds containing carbon, while all other chemicals are inorganic. Inorganic nutrients include nutrients such as iron, selenium, and zinc, while organic nutrients include, among many others, energy-providing compounds and vitamins. A classification used primarily to describe nutrient needs, divides nutrients into macronutrients and micronutrients. Consumed in relatively large amounts (grams), macronutrients (carbohydrates, fats, proteins) are primarily used to generate energy or to incorporate into tissues for growth and repair. Micronutrients are needed in smaller amounts (milligrams or micrograms); they have subtle biochemical and physiological roles in cellular processes, like vascular functions or nerve conduction. Inadequate amounts of essential nutrients, or diseases that interfere with absorption, result in a deficiency state that compromises growth, survival and reproduction. Nevertheless, the Mediterranean diet refers to naturally occurring foods native to Greece, Italy and Spain before globalization of food products in the 20th century. The diet includes relatively high consumption of fruit, vegetables, olive oil, legumes, whole grains and moderate amounts of red wine. Foods with increased fat and dairy are minimally consumed. Some nutritional genomics studies have pointed towards the Mediterranean diet to be most nutritionally beneficial. It has been positively linked towards decreased mortality by providing protective agents against metabolic diseases, cardiovascular disease and several types of cancer. These benefits have been attributed to the abundance of dietary compounds present in Mediterranean foods. Examples of this include turmeric, lycopene, and polyphenols in extra virgin olive oil. It has been suggested that each of these allegedly bioactive compounds, along with several others, interacts with the body's cellular and molecular function, gene expression and epigenome to prevent angiogenesis and the development of neurodegenerative disease.

Genetic is the study of heredity and genetic variation in living organisms, while Genomics is distinct from genetics. **Genomics** is the study of genes and their functions, and related techniques. Moreover, genomics is the study of the total or part of the genetic or epigenetic sequence information of organisms, and attempts to understand the structure and function of these sequences and of downstream biological products. Furthermore, genetics may look at a single gene, while genomics looks at all genes and how they interact with other genes to influence growth and development of organism. The creation of **nutrigenomics and nutrigenetics, two fields with distinct approaches to elucidate the interaction between diet and genes** but with a common ultimate goal to optimize health through the personalization of diet, provide powerful approaches to unravel the complex relationship between nutritional molecules, genetic polymorphisms, and the biological system as a whole. DNA usually occurs as linear chromosomes in eukaryotes. The set of chromosomes in a cell makes up its genome. The information carried by DNA is held in the sequence of pieces of DNA called genes. Transmission of genetic information in genes is achieved via complementary base pairing. For example, in transcription, when a cell uses the information in a gene, the DNA sequence is copied into a complementary RNA sequence through the attraction between the DNA and the correct RNA nucleotides. Usually, this RNA copy is then used to make a matching protein sequence in a process called translation, which depends on the same interaction between RNA nucleotides. In alternative fashion, a cell may simply copy its genetic information in a process called DNA replication. Furthermore, genetic is the study of genes, genetic variation, and heredity in living organisms. The branches of genetics are the classical, molecular, population, quantitative, cytogenetics, ecological, developmental, microbial, behavioral genetics and genetic engineering. Classical Genetic is the study of the mechanisms involved in the passage of genes from one generation to the next. Molecular Genetic is a sub-field of biology that addresses how differences in the structures or expression of DNA molecules manifest as variation among organisms. Molecular genetics often applies to determine the structure and / or function of genes in an organism's genome. Population genetics use the frequencies of different alleles of a gene in populations, and combine them with concepts from simple Mendelian inheritance to analyze inheritance patterns across generations and descendant lines. Also, population genetics focus on particular genes and their subsequent metabolic products. Quantitative Genetic deals with quantitative traits, which are phenotypes that vary continuously (such as milk yield) as opposed to discretely identifiable phenotypes and gene-products (such as black vs. brown eyes). Genomics is an interdisciplinary field of biology focusing on the structure, function, mapping, and editing of genomes. A genome is an organism's complete set of a DNA, including all of its genes. In contrast to genetics, which refers to the study of individual genes and their roles in inheritance, genomics aims at the characterization and quantification of all of an organism's genes, their interrelations and influence on the organism. Genes expression direct the production of proteins with the assistance of enzymes. Genomics also involves the sequencing and analysis of genomes through uses of high through DNA sequencing and bioinformatics to assemble and analyze the function and structure of entire genomes. The field also includes studies of intragenomic (within the genome) phenomena such as epistasis (interaction among various genes), pleiotropy (one gene affecting more than one trait), heterosis (hybrid vigor, superiority of offspring compared to parents), and other interactions between loci and alleles within the genome. Improvement performance of living organisms (including human, agriculture and livestock), the clinical applications of genomic technologies, gene discovery and diagnosis of rare monogenic disorders, identification and diagnosis of genetic factors contributing to common disease. In intensive livestock systems, genomic data enhances existing genetic improvement programs by increasing the accuracy of estimates of relationships among animals. Moreover, Genomics is

animal breeding aims to use DNA (Genotype) to help better predict how well an animal will perform in the future. Genetic improvement has the potential to assist in meeting market requirements. Improve overall productivity and profitability. Improve specific traits of a flock including reproductive performance, growth rate, carcass yield, and milk production.

Nutritional genomics, also known as **nutrigenomics**, is a science studying the relationship between living organisms (human and animals) genome, nutrition and health. People in the field work toward developing an understanding of how the whole body responds to a food via systems biology, as well as single gene/single food compound relationships. Nutritional genomics or Nutrigenomics is the relation between food and inherited genes, it was first expressed in 2001. nutrigenomics explains some aspect of how genes react to nutrients and express specific phenotypes, like disease risk. There are several applications for nutritional genomics, for example how much nutritional intervention and therapy can successfully be used for disease prevention and treatment.

Gene expression is the process by which information from a gene is used in the synthesis of a functional gene product that enables it to produce end products or, protein or non-coding RNA, and ultimately affect a phenotype (observable trait), as the final effect. These products are often proteins, but in non-protein-coding genes such as transfer RNA (tRNA) and small nuclear RNA (snRNA), the product is a functional non-coding RNA. The process of gene expression is used by all known life eukaryotes (including multicellular organisms, including human and animals), prokaryotes (bacteria). In genetics, gene expression is the most fundamental level at which the genotype gives rise to the phenotype (observable trait). The genetic information stored in DNA represents the genotype, whereas the phenotype results from the "interpretation" of that information. Such phenotypes are often displayed by the synthesis of proteins that control the organism's structure and development, or that act as enzymes catalyzing specific metabolic pathways. All steps in the gene expression process may be modulated (regulated), including the transcription, RNA splicing, translation, and post-translational modification of a protein. Regulation of gene expression is the basis for cellular differentiation, development, morphogenesis and the versatility and adaptability of any organism.

2 Human Health

Food intake and the environment are the two main factors that affect the health or illness of an individual. Studies in nutritional area have increased the understanding of how to maintain healthy a group of individuals that live in different dietary conditions. However, after the conclusion of the Human Genome Project (HGP), new insights about the influence of nutrients into people's diet were postulated, which included:

- Will gene expression in response to metabolic process, at cellular level, influence the health of an individual?
- Are gene expression and metabolic response the result of the interaction between genotype and environment/nutrient?
- Understanding how this interaction process occurs between gene and nutrient could lead to the prescription of specific diets for each individual.

During the 19th century, studies on metabolism and chemistry were done, helping the science of nutrition on defining their role in the development and prevention of chronic diseases, such as cancer, cardiovascular, neurodegenerative, and bone metabolism disorders. Nowadays, the “Pos-Genomic Era” is being experienced. This era is characterized by the integration of three fields: biological, social, and environmental, where scientific discoveries on nutritional pathophysiology and metabolism are included. After the HGP, discussions and actions began on a new biological era, the “Post-Genomic Era”, where the evolution of bioinformatics provided advances in “omics” science research. These sciences use biotechnology to isolate and characterize a greater number of biomolecules from the same group, such as DNA, RNA, proteins, or metabolites. Hence, after Genomics, other biological Sciences appeared as revolutionary tools, such as Proteomics, Metabolomics and Transcriptomics. Therefore, the first definition of nutrigenomics referred only to studies on the effects of nutrients/bioactive food on gene expression of an individual. Nowadays, this definition expanded and, recently, nutrigenomics also involves the studies on nutritional factors that act protecting the genome. Thus, this new science seeks to understand the influence of dietary components on the Genome, Transcriptome, Proteome, and Metabolome. Nutrigenomics, in a single experiment, can generate multiple responses, so it is necessary to be innovative in the approaches of this area. Moreover, Nutrigenomics is able to extract useful biological information from the data collected. The final answer can only be achieved after a series of investigations or surveys among different groups and teams. Therefore, there is a growing partnership between countries/teams/research groups, involving Nutrition field, Biology, Medicine, Genomics, and Bioinformation. The studies on nutrigenomics are focused on the effects of the nutrients over the genome. The search for knowledge regarding healthy/adequate food has increased in the last decades among the world population, researchers, nutritionists, and health professionals. Since ancient times, humans have known that environment and food can interfere with an individual's health condition, and have used food

and plants as medicines. With the advance of science, especially after the conclusion of the Human Genome Project (HGP), scientists started questioning if the interaction between genes and food bioactive compounds could positively or negatively influence an individual's health. With information obtained from the HGP, it was found that humans have 99.9% identity between their genomes. A distinct difference between their weight, height, eye color/hair, and other features is only 0.1% of the gene sequence and this difference, among other factors, also determines the nutritional requirements and the risk of developing some of the NTCDs. Single Nucleotide Polymorphisms (SNPs) are the main reason for this genetic variation, and it can often change the encoded protein. Studies have shown that certain genes and their variants can be regulated or are influenced by nutrients/food compounds from the diet and that these molecular variations may have beneficial actions to the health of an individual. In order to assess this interaction between genes and nutrients, the term “Nutrigenomics” was created. Hence, Nutrigenomics corresponds to the use of biochemistry, physiology, nutrition, and genomics to seek and explain the existing reciprocal interactions between genes and nutrients at a molecular level. Therefore, nutrigenomics is the area of nutrition that uses molecular tools to search, access, and understand the several responses obtained through a certain diet applied between individuals or population groups. It seeks to elucidate how the components of a particular diet (bioactive compound) may affect the expression of genes, which may have increased its potential or which can be suppressed. This response will depend on how genes will show a changed activity or alter gene expression. Some examples of this gene-nutrient interaction are their capacity on binding to transcription factors. This binding enhances or interferes with the ability of transcription factors on interacting with elements that will lead to the binding control of RNA polymerase. Earlier studies performed with vitamins A, D and fatty acids have shown that they can trigger direct actions in activating nuclear receptors and induce gene transcription. Compounds such as resveratrol present in wine and soy genistein may indirectly influence the molecular signaling pathways, such as the factor kappa B. The involvement of these factors in the activation and regulation of key molecules is associated with diseases ranging from inflammation to cancer. The discovery of these interactions (gene-nutrient) will aid the prescription of customized diets according to each individual's genotype. Thus, it will be possible to mitigate the symptoms of existing diseases or to prevent future illnesses, especially in the area of Nontransmissible Chronic Diseases (NTCDs), which are currently considered an important world public health problem. Nutritional science originally emerged as a field that studied individuals lacking certain nutrients and the subsequent effects, such as the disease, which results from a lack of nutrients. Also, diseases closely related to diet (but not deficiency), such as obesity, became more prevalent, nutritional science expanded to cover these topics as well. Nutritional research typically focuses on preventative measure, trying to identify what nutrients or foods will raise or lower risks of diseases and damage to the human body. The applications of nutritional genomics are multiple. With personalized assessment some disorders (diabetes, metabolic syndrome) can be identified. Nutrigenomics can help with personalized health and nutrition intake by assessing individuals and make specific nutritional requirements. The focus is in the prevention and the correction of specific genetic disorders. Examples of genetic related disorders that improve with nutritional correction are coronary heart disease (CHD), obesity, hypertension and diabetes mellitus type 1.

3 Coronary heart disease (CHD)

Genes tied to nutrition manifest themselves through the body's sensitivity to food. In studies about CHD, there is a relationship between the disease and the presence of two alleles found at E and B apolipoprotein loci. These loci differences result in individualized reactions to the consumption of lipids. Some people experience increased weight gain and greater risk of CHD whereas others with different loci do not. Research has shown a direct correlation between the decrease risk of CHD and the decrease consumption of lipids across all populations.

3.1 Obesity

Obesity is one of the most widely studied topics in nutritional genomics. Due to genetic variations among individuals, each person could respond to diet differently. By exploring the interaction between dietary pattern and genetic factors, the field aims to suggest dietary changes that could prevent or reduce obesity. There appear to be some SNPs that make it more likely that a person will gain weight from a high fat diet; for people with AA genotype in the FTO gene showed a higher BMI compared those with TT genotype when having high fat or low carbohydrate dietary intake. The APO B SNP rs512535 is another diet-related variation; the A/G heterozygous genotype was found to have association with obesity (in terms of BMI and waist circumference) and for individuals with habitual high fat diet (>35% of energy intake), while individuals with GG homozygous genotype are likely to have a higher BMI compared to AA allele carriers. However, this difference is not found in low fat consuming group (<35% of energy intake).

3.2 Cancer

The need for certain micronutrients by the organism depends on the person's age, genetic background, and physical state. Earlier studies showed that the deficiency of micronutrients, such as folic acid, vitamins B12, B6, C, and E,

selenium, niacin, and zinc can cause changes into the DNA similar to what is seen after radiation exposure. These alterations can lead to the rupture of the DNA double strand, oxidative lesions, or both. Furthermore, they demonstrated to be narrowly related to the development of cancer. Moreover, molecules present in contaminated food can produce toxic metabolites that may interact with DNA, modifying its structure and inducing mutations. It is the case of aflatoxin B1, which forms an adding compound able to bind to the N-7 position of guanine residue, generating a new product. This new molecule cleaves, then, the interaction between one sugar and one nitrogenous base of a nucleotide, leading to the formation of an apurinic site. The mutation can, thus, cause severe damages on the liver, including necrosis, cirrhosis, and carcinoma. During the metabolism of folate, the folic acid found in food sources, is absorbed by the intestine and, through many chemical processes of catabolism and synthesis, it is transformed into 5-methyltetrahydrofolate. This chemical component is necessary for the synthesis of methionine, which in turn is used during the process of DNA mutilation. Thus, a diet poor in folic acid can alter this process and interfere on DNA replication, leading also to an increased risk of cancer development. Nevertheless, various minerals work as protectors against cancer development. Among them, there are:

- Selenium, which stimulates the production of glutathione peroxidase enzyme that acts on the reduction of hydrogen peroxide and maintain the integrity of cell membranes;
- Prostacyclins, which decrease the oxidative damage of important molecules, such as dna, lipids, and lipoproteins;
- Zinc, which act on processes for the maintenance of genomic stability, genetic expression, and apoptosis modulation.

Similarly, it is estimated that diet influences about 30–40% of all cancer cases, many studies indicate that breast, prostate, liver, colon and lung cancers are linked to the dietary intakes. One interesting example of the complex interactions between genetics, diet and disease is from a study on the occurrence of hepatocellular carcinoma in Sudanese population. It was perceived that a stronger relationship existed between the risk of developing the disease and the consumption of peanut butter contaminated with aflatoxins in Sudanese people with the glutathione *S*-transferase M1 null genotype compared to those lacking this genotype. So far, more than 1000 different phytochemicals have been recognized with cancer preventive activities. Several dietary compounds such as selenium, epigallocatechin-3-gallate, phenylethyl isothiocyanate, retinoic acid, sulforaphane, curcumin, apigenin, quercetin and resveratrol have their cancer preventive effect by apoptosis inhibition. During chronic inflammation, several changes have been observed in cells including increased DNA damage, disruption of DNA repair pathways, cellular proliferation, inhibition of apoptosis, and promotion of angiogenesis and invasion. Cancer metabolism has unique attention due to its involvement in every stage of cancer development. Cancer cells are characterized by an altered metabolism to maintain their rapid enormous growth. Omega-6 and omega-3 PUFA have been proven to differentially influence gene expression linked to inflammation (e.g. TNFα, IL-1β, IL-6, IL-18), angiogenesis (e.g. VEGF, PDGF, IGF-1, MMP-2), and proliferation (e.g. cyclin, p53, Wnt, PTEN) and can thereby control tumorigenesis. The crucial role of nutrigenomics in the field of cancer therapy still needs more research.

3.3 Type II Diabetes

Diabetes counts for more than 90% of all diseases of the world. Type II Diabetes is a multifactorial pathogenesis that involves the interaction between genetics and environmental factors. Genomics studies showed that there are 65 SNPs associated with the risk of developing type II Diabetes. With the advances of genome sequencing and the decoding of the human genome, tests for the detection of SNPs related to Type II Diabetes became available to the public. In these exams, the patient is able to know it there is a genetic predisposition to develop the disease. However, caution must be taken on applying this test for clinical practice, once that studies have shown that patients that had negative results on this exam for the presence of Type II Diabetes SNPs felt so secure about it that they stopped taking care of their food diets. Consequently, some later developed Diabetes due to food income and insulin tolerance. Nevertheless, patients who received a positive result for the presence of type II Diabetes change their life style, especially in their food intake, which later decreased the development of the disease by this group.

3.4 Lactose Intolerance

An inability to digest lactose, a type of sugar found naturally in milk and milk products. This causes diarrhea, and bloating after consuming milk or dairy products. It happens when people small intestine does not produce enough lactase, an enzyme that breaks down lactose. Lactose intolerance is genetically influenced by the expression of the LCT gene, which is controlled by a DNA sequence near the MCM6 gene. Some people have a genetic trait that decreases the expression of the LCT gene after infancy, leading to lactose intolerance, while others have a genetic variation that persists the expression of the LCT gene, allowing them to digest lactose. In lactose intolerance, digestive symptoms are caused by lactose malabsorption, a condition in which the small intestine cannot digest, or break down, all the lactose.

Different people can tolerate different amounts of lactose before having symptoms. Lactose malabsorption is more common in some parts of the world than in others. In Africa and Asia, most people have lactose malabsorption. In some regions, such as northern Europe, many people carry a gene that allows them to digest lactose after infancy, and lactose malabsorption is less common. In the United States, about 36 percent of people have lactose malabsorption. Lactose intolerance may affect human health if it keeps them from getting enough nutrients, such as calcium and vitamin D. Milk and milk products, which contain lactose, are some of the main sources of calcium, vitamin D, and other nutrients.

4 Nutrigenomics and Nontransmissible Chromic Diseases (NTCDs)

Nutrition is the process that offers different substances to an organism that can work as energy supplier (carbohydrate and fat), as cell structure sources (proteins), and on metabolism control (vitamins and minerals), thus maintaining its homeostasis. The nutritional state of an individual is the result of the interaction between various factors, such as genetic background, physical body, and emotional and social state. Diet is a key role factor, once those nutrients and other bioactive compounds present in food can either be beneficial or initiate several diseases. Among the illnesses related to food consumption, there are the celiac disease, phenylketonuria, and NTCDs, such as cancer, and diabetes. In this way, the health state of a person will depend on the interaction between their genes and their food diet. Therefore, Nutrigenomics, along with other biological sciences, aim to clarify the interaction between genes and bioactive compounds from food sources.

4.1 Phenylketonuria

Phenylketonuria, otherwise known as PKU, is an uncommon autosomal recessive metabolic disorder that takes effect postpartum but the debilitating symptoms can be reversed with nutritional intervention.

5 Future Prospect of Genomic Techniques for Improvement Livestock Performance

The rearing of farmed animals is a vital component of global food production systems, but its impact on the environment, human health, animal welfare, and biodiversity is being increasingly challenged. Developments in genetic and genomic technologies have had a key role in improving the productivity of farmed animals for decades. Advances in genome sequencing, annotation, and editing offer a means not only to continue that trend, but also, when combined with advanced data collection, analytics, cloud computing, appropriate infrastructure, and regulation, to take precision livestock farming (PLF) and conservation to an advanced level. Such an approach could generate substantial additional benefits in terms of reducing use of resources, health treatments, and environmental impact, while also improving animal health and welfare. The genetics of livestock are a critical factor influencing animal production and health. Genomics makes clear what was once unknown. Genomic testing can help predict future profitability potential of animals. This in turn allows producers to optimize the profitability and yields of their herds by making different animal selection and strategic breeding decisions. The genomic sequences for most livestock species in the 21st century have generated the potential to revolutionize livestock production globally, by providing farmers with the ability to match individual animals to the requirements of rapidly changing climates, production systems and markets. The technology which has had the greatest impact to date is genomic selection. Genomic selection uses information from a large number of genetic markers or single nucleotide polymorphisms (SNPs) in conjunction with measurements (phenotypes) of important traits in livestock to estimate breeding values, without requiring precise knowledge of where specific genes are located in the genome. Since the principles of genomic selection were initially proposed in 2001, genomic selection has been widely adopted in animal breeding programs globally because of its ability to improve selection accuracy, reduce generation intervals and increase genetic gains. It has transformed the livestock industry. Genomic technology in animal production has a growing number of practical benefits, such as in the production of transgenic animals resistant to disease, increasing the productivity of animals, in the treatment of genetic disorders, and the production of vaccines. The information in an organism's genes provides a biological blueprint for its appearance, function and survival and largely defines its similarities and differences with other organisms. Now more than ever, such remarkable improvements in yields of animal protein are needed to meet the ever-increasing demand for animal protein around the world. However, achieving genetic improvement in modern-day animal agricultural systems comes with its own complexities. Using cutting-edge research techniques, animal geneticists are making progress toward understanding the precise genetic factors that promote health and regulate growth, reproduction, and nutrient utilization. This foundational knowledge will lead to new tools and management practices and enable increased production while reducing impacts of animal agriculture on the environment. Recent initiatives in animal genomics are directed toward deciphering the genetic code of food-producing animals. The resulting genomic technologies will enhance our efforts to identify the genes and genetic mechanisms underlying economically important traits in livestock species.

6 Nutrigenomics and Nutrigenetics in the Process of Milk Production

New thoughts of study, dealing with of allele/gene expression that incorporates two distinct fields of studies called nutrigenomics and nutrigenetics has been created in latest years. Nutrigenomics is described as the research of "genome-wide nutritional factors" and how this "influences the equilibrium between performance, and health by changing the genetic makeup of an individual's expression and/or structure". Nutrigenomics in dairy cows is a relatively new area of research. It is defined as the study of the genome-wide influences of nutrition altering the expression of genes. Dietary compounds affect gene expression directly or indirectly via interactions with transcription factors. Among those, the most relevant for nutrigenomics are ligand-dependent nuclear receptors, especially peroxisome proliferator-activated receptors (PPAR) and liver X receptor. Among other transcription factors, a prominent nutrigenomic role is played by the sterol regulatory binding protein 1 (SREBP1). Data from studies on dairy cows using gene expression and gene reporters among the main molecular methods used to study nutrigenomics in dairy cows, are indicative of a network of multiple transcription factors at play in controlling the nutrigenomic responses. Fatty acids, amino acids, and level of feed and energy intake have the strongest nutrigenomic potential. The effect of t10, c12-conjugated linoleic acid on depressing milk fat synthesis via inhibition of SREBP1 was among the first and likely the best-known nutrigenomic example in dairy cows. Although long-chain fatty acids (LCFA) are clearly the most potent, a nutrigenomic role for short-chain fatty acids is emerging. Available data indicate that saturated compared with unsaturated LCFA have a more potent nutrigenomic effect in vitro, likely through PPAR. In vivo the effect of saturated LCFA is more modest with contrasting effects among tissues. A more complete understanding at a molecular level (i.e., mRNA abundance) of the regulation of milk fat synthesis and secretion by LCFA would contribute to the development of nutrigenomics strategies to alter milk FA composition and optimizing milk fat production in dairy ruminants. In non-ruminants, LCFA interact directly with transcription regulators such as PPAR, LXR, and hepatic nuclear factor (i.e., HFN-4α) to elicit a response. However, the activation of PPARγ by LCFA was not demonstrated but only inferred. Furthermore, prior data were indicative of a lower response to rosiglitazone in goat mammary cells compared to bovine mammary cells. Thus, the specific roles of LCFA in the regulation of milk fat synthesis via modulation of PPARγ in ruminant mammary cells and, more so, in goat mammary cells, remains unclear. Gene reporter technology (GRT) has opened several new avenues for monitoring biological events including the activation of transcription factors, which are central to the study of nutrigenomics. However, this technology relies heavily on the insertion of foreign plasmid DNA into the nuclei of cells (i.e., transfection), which can be very challenging and highly variable among cell types. Compared with bovine mammary cells, goat mammary cells appear less responsive to rosiglitazone. This was previously demonstrated using gene reporter data and supported by the lower number and magnitude of transcripts affected by rosiglitazone in our experiment compared with MACT cells. It is noteworthy that the protein sequence of PPARγ is highly conserved between bovine and goat, considering that 99.6% of amino acid sequence is identical when compared using Pairwise Sequence Alignment (LALIGN) and the ligand-binding domain has 100% conservation. Moreover, other genes related to lipid metabolism were also downregulated in both CLA-and FO-MFD when these conditions were compared to the control, such as some genes associated with activation of acetoacetate to acetoacetyl-CoA (AACS), activation of fatty acids with CoA (ACSS2, ACSS3), and desaturation of fatty acids (FADS2). Expression of most of these lipogenic genes is controlled by the sterol regulatory element-binding protein-1 (SREBP1) signaling pathway, which was found to be inhibited in our previous study comparing the transcriptomes of FO-MFD and control ewes. In addition to the differences between the mechanisms of action of CLA and FO, these downregulated genes suggest there are common pathways activated in both types of diet-induced MFD. Although both SREBF1 and SREBF2 have been associated with lipid metabolism in the mammary gland, each isoform may have different roles. Thus, SREBF2 would be mainly involved in cholesterol biosynthesis, whereas SRBEP1 signaling would be crucial to MFD. As mentioned above, several genes clustered in this pathway were found to be down regulated in CLA and FO, but these did not include SREBF1. As mentioned above, several genes clustered in this pathway were found to be down regulated in CLA and FO, but these did not include SREBF1. The complex posttranscriptional regulation of SREBF1, as well as the relatively advanced stage of lactation, may be of relevance in this regard. Although the mechanisms of action of the trans-10, cis-12 CLA isomer that reduce milk fat are not clear yet, scientific evidence points to the fact that this process is regulated by suppression of nuclear fragments in the sterol regulatory element-binding protein 1(SREBP1). SREBP1 is a global regulator of milk fat synthesis , involved in the regulation of lipogenic genes in mammary epithelial tissue, particularly with those associated with de novo synthesis. In this regard, the degree of SREBP1 suppression is directly proportional to the magnitude of the fall in milk fat caused by the trans-10, cis-12 CLA isomer. Nutrigenomic effects of amino acids are emerging, particularly for the regulation of milk protein synthesis-associated genes. The level of energy in the diet has a strong and broad nutrigenomic effect and appears to 'prime' tissue metabolism, particularly liver. The frontier of the nutrigenomics era in ruminants and initial data strongly indicate that this scientific branch (nutriepigenomics) can play a critical role in future strategies to better-feed dairy cattle. Nutrients have profound effects on gene expression and differentiation of cells in general. Research is becoming more and more active in this field, which forms an exciting new research field called nutrigenomics (Table 1).

Table 1 Nutrients effects on gene expression

Gene name	Gene symbol	Nutrient	Function
Retinoid X receptor, beta	RARA	Retinoic acid	Morphogenesis embryonic, cell growth and differentiation
Retinoid X receptor, gamma	RARA	Retinoic acid	Growth and development of the skeleton
Peroxisome proliferatoractivated receptor, alpha	PRARA	Fatty acids	Fatty acid metabolism, inflammation, and tissue regeneration
Vitamin D receptor	VDR	Vitamin D	Immune response

Dairy genetics help predict how characteristics such as milk production, increased milk total solids (protein, fat, lactose, minerals and vitamins) or health and management traits are passed onto the next generation of cows. The effect of breeding decisions is cumulative, meaning they build over the generations and have a key role to play in farm profitability. Moreover, many genes are involved in milk components synthesis. Genes are activated by feed nutrients. One of the most comprehensive and successful examples of nutrigenomics in current animal science studies is the study of milk fat synthesis and its regulation by distinctive bioactive fatty acids. Therefore, the most powerful nutrigenomic compounds in the diet are the fatty acids. Other dietary elements have nutrigenomic roles, including the rate of nutrient consumption that can be used to prime the liver (and other tissues) to better meet metabolic difficulties, and AA, whose original studies disclosed an exciting nutrigenomic function in regulating the synthesis of milk protein. Milk cow has a small percentage of fat content (about 3% – 4%), with linoleic acid and linolenic acid predominantly PUFAs. The ester connections are hydrolyzed when nutritional lipids reach the rumen (> 85 percent) followed by unsaturated FA biohydrogenation. Biohydrogenation is a conversion by rumen bacteria of unsaturated to saturated fatty acids. This intensive conversion also results in the creation of a number of conjugated linoleic acids and fatty acids trans 18:1, some of which are bioactive in the ruminant and other species when taken up by the mammary glands. Biohydrogenation includes only a few species of rumen bacteria and performs these responses as a system for protecting against PUFA's poisonous impacts and/or matching the FA profile required for microbial development. Rumen outflow of FA is primarily saturated free FA as a result of this comprehensive hydrolysis and biohydrogenation. Recent studies in mammals such as rodents, cows, and humans have shown that lipids can control gene expression in the liver and mammary gland, helping to maintain adequate saturated fatty acids (SFA), monounsaturated fatty acids (MUFA), and polyunsaturated fatty acid (PUFA) levels in these tissues. Dietary lipids can function as lipogenesis regulators that interact with transcription factors including peroxisome proliferator-activated receptor (PPAR) and sterol-regulatory element binding protein (SREBP) transcription variables. Meanwhile, milk protein yield is of great significance for the dairy industry. The main proteins in milk are caseins and whey proteins (i.e., alpha-lactalbumin, beta-lactoglobulin, whey acidic protein (WAP), albumin, and immunoglobulin; proteins highly enriched in the milk serum after removal of casein). The milk fat globule membrane (MFGM) is also highly enriched with proteins even though those account for only 1-4% of total protein in the milk. Results of research identified 120 proteins in a proteomics analysis of the bovine MFGM. The amount and composition of proteins in milk is largely determined by the genetics of the animal, and is difficult to change through nutrition. However, due to the high requirement of protein synthesis for energy, the milk protein yield can be affected by the energy content in the diet.

7 Conclusion

Human DNA influence the need for specific nutrients for maintaining good health throughout life. Therefore, it is helpful to determine the personalized diet requirements based on the genetic makeup of the person to clarify some etiological perspectives of chronic diseases, because of the associations between diet and chronic diseases.Compliance with ethical standards.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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