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3.36 Personalized Nutrition and -Omics

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3.36.1 Introduction

In the changing era of development in all branches of science, health, economics and technology, the ever increasing population and environmental issues brings new challenge to modern world. Increasing use of chemicals in various life activities, agriculture and food sectors, have resulted into various kind of negative effects on human health. There are well-known reports of treating various health elements using traditional practices, plant extracts and specific food types (Vyas et al., 2018). Advances in analytical technology is one of the major breakthrough for determining key components of food and attracted economically sound consumers to eat food with better nutrient composition. It has resulted into development of numerous food products with targeted consumers of different age groups, health and economic status etc. Development in genome sequencing technologies and sequencing of human genome has provided enormous opportunities for study of gene-diet interaction. In this chapter, we have discussed about concept of personalized nutrition, factors contributing to this trend and related technological aspects in following sections.

3.36.2 Personalized Nutrition: Concept and Importance

It is a well-established truth that dietary factors are the contributors to many of the common diseases, specially heart ailments, type II diabetes, cancer etc (Micha et al., 2017). This fact suggests the personalization of dietary habits that may be more impactful in changing behavior and ultimate health outcomes (Ordovas et al., 2018). Personalized nutrition is rather defined as an approach that counts on details of an individual characteristics to evolve a package of nutritional counsel, products, or services. Gibney et al. (2016), explained it as a perspective “assists individuals in achieving a lasting dietary behavior change that is beneficial for health”. The terms such as precision nutrition, nutrigenomics (Vyas et al., 2018), personalized tailored nutrition and stratified nutrition partially imbricates with personalized nutrition. Some of the terms can be used synonymously as personalized nutrition and personalized tailored nutrition. Both the terms imply to convey suitable nutritional advice to respective individual. Similarly, when a well suited nutritional advice is delivered to respective group it is termed as stratified or tailored. Whereas nutrigenomics implicate characterization of gene products influenced by nutrient intake and their resulted metabolic consequences (Ordovas et al., 2018). Zeisel (2020), has recommended and justified the use of term “precision nutrition” rather than “personalized nutrition” because the concept has even greater potential to categorize the whole population in different groups based on biomarkers studies.

Comprehensively, personalized nutrition is the associated individual's genetic, phenotypic, medical, nutritional, and other important information's which is intended to pitch specific healthy eating and nutritional guidance as per need. There may be parallel appliance of diet management under personalized nutrition for patients or who require particular nutritional composition like lactating mothers, pregnant woman or old age and to healthy persons for ameliorating public health. People with special personal goals as for achieving wanted body shape or size, competitive sports and for dealing with preferences, also desire to get benefitted by personalized nutrition (Pickering and Kiely, 2018). In case of personalized nutrition, genotypic or phenotypic characteristics have been focal point of the most researchers and stakeholders. Deducible suggestion is that, the outcomes of personalization will be more effective with the diverse measurements of characteristics (Riedl et al., 2017). This kind of adopted lifestyle highly rely on effective collaboration with participants to take responsibility for their behavior, and subsequently of their health (Macready et al., 2018).

3.36.3 Driving Factors for Increasing Concern/Advances in Personalized Nutrition

3.36.3.1 Advances in Food Analytics

Food analysis is continuously evolving analytical methodologies that deals with development of more vigorous, productivity and sensitivity techniques at low cost along with assurance of safety, quality, and traceability of foods in consent with Food laws and individual needs of the consumer. McGorin (2009) exhibited it as *"the growth and infrastructure of the modern global food distribution system heavily relies on food analysis (beyond simple characterization) as a tool for new product development, quality control, regulatory enforcement, and problem-solving."* Though, at present and in near future, there is huge demand of health-related properties of foods due to intensified public interest for improving health and to have a disease-free life through functional foods and nutraceuticals in conjunction with foodomics.

In general, working principle defines the classification of the analytical techniques. Every single technique projected to provide peculiar information about the sample components on the basis of specific physicochemical interactions. Numerous techniques are available for analytical purposes which might be spectroscopy including mass spectrometry (MS); nuclear magnetic resonance (NMR); infrared (IR) and atomic spectroscopy (AS); ultra-violet and visible light spectroscopy; fluorescence spectroscopy; circular dichroism spectroscopy (CD), for separation of various food components through high-performance liquid chromatography (HPLC); gas chromatography (GC); ion-exchange chromatography (IEC); electrophoresis; supercritical fluid chromatography (SFC), biological comprise of polymerase chain reaction (PCR); for extraction and preparation of sample via solid phase extraction (SPE); supercritical fluid extraction (SFE); flow injection analysis (FIA); purge and trap (PAT); microwave-assisted extraction (MAE); automatic thermal desorption (ATD), hyphenated by collective combination of separation and spectroscopic techniques, immunological techniques and biosensors, electrochemical techniques etc. For determining health effects of foods, various immunological techniques such as enzyme immunoassay (EIA), enzyme-linked immunosorbent assay (ELISA), immune radiometric assay (IRMA), fluorescence: fluorescence immunoassay, enzyme-linked fluorescent immunoassay, fluorescence polarization immunoassay (FPIA), time-resolved fluorescence immunoassay (TRFI), chemiluminescence immunoassay (CIA), immune dotting, radioimmuno assay (RIA), solid-phase RIA and liquid-phase RIA etc. has been developed (Cifuentes, 2012).

One of the major thrust areas in the application of specific analytical techniques to solve various problems associated with food analysis is the development of sample preparation techniques, due to complex nature of foods. This being the fundamental step in the evolution of any new analytical methodology, research and development of new sample preparation procedures is the most attractive section. Sophisticated sample preparation techniques aims to decrease use of laboratory solvent and generation of hazardous waste material to minimize labor, time, and the cost per sample analyzed, along with improving the overall efficacy the analyte isolation. This involves the development and potential use of molecularly imprinted polymers in sample preparation (Lok and Son, 2009), the utilization of monoliths in sample preparation and analysis (Samanidou and Karageorgou, 2011), the application of immune affinity column clean-up techniques in food analysis (Senyuva and Gilbert, 2010), the addition of solid-phase micro extraction (SPME) techniques for quality characterization of various food products (Balasubramanian and Panigrahi, 2011), the use of ultrasound-assisted extraction for estimation of contaminants in food (Tadeo et al., 2010), and the application of liquid phase micro extraction in food analysis etc (Asensio-Ramos et al., 2009). Presently, novel greener sample preparation methodologies are being developed; among them, supercritical fluid extraction (SFE) and subcritical water extraction (SWE) are more encouraging processes in food analysis (Aufartová et al., 2011), and for attaining new ingredients of functional foods. The basis of these extraction techniques are the use of pressurized fluids which gives electivity, shorter extraction times, and environmentally friendly as well.

The major developments of novel techniques have been brought about by recent advances in the following:

- a) Molecular methods and DNA based techniques permits faster and precise detection of bacteria in foods, microbial composition of various foods and multiple genetically engineered crops which is still a crucial area. The effect of food processing on degradation of plant DNA and PCR-based analysis of transgenic foods are also studied (Gryson, 2010).
- b) Biosensors are regarded as analytical devices which are composed of a specific biologically recognized element e.g., enzymes, antibodies, and microbe, combined with a specific transducer (chemical or physical) that converts the chemical response into an electrical signal. Biosensor transduces continuous or semi-continuous electronic signals proportionate to an analyte or cluster of analytes. Biosensors have been routinely used to detect food components, preservatives, food colors and sweeteners, along with

contamination of toxins, pesticides, antibiotics, hormones and microbial etc. Due to such advantages biosensors found a huge scope in food processing, and food quality certification. The recent development and application of electronic nose or electronic tongue that imprints a large impact on flavor analysis are the best examples of it. Application of biosensors is increasing tremendously by virtue of rapid response time, high precision, sensitivity, and the utilization in inline process monitoring or food manufacturing.

- c) The use of peptide nucleic acid (PNA)-based technologies for food authentication and analysis, the progression of novel immunoassay methodologies to analyze veterinary drug residues in food products and the characterization of plant food allergens are owing to the methodology development.

In the post-genomic era with the sequencing of approximately whole human genome, terms such as “foodomics”, “personalized nutrition”, “nutrigenomics” came into consideration as novel domains which incorporate advanced omics techniques for absolute improvement in public health, well-being and knowledge (Cifuentes, 2009; Zeevi et al., 2015). The purpose to use such novel terms in the post-genomic era with respect to food analysis is to feature challenges under traditional and current investigation can find new key by using epigenomics, genomics, transcriptomics, proteomics, and metabolomics tools.

3.36.3.2 Nutrition Based Diseases and Public Health Programs

3.36.3.2.1 Occurrence of Diet and Nutritional Based Chronic Diseases

Nutrition base disease is a condition that causes illness in humans. There may be excess or deficiencies of nutrients in diet which may lead to eating disorders, obesity and chronic diseases like cardiovascular disease, hypertension, cancer, and diabetes mellitus. Various nutrient-deficiency based diseases are presented in the **Table 1** below with the symptoms and respective nutrient rich diet.

Chronic diseases progress over prolonged period of time and takes time to resolve properly. The relation between diet and chronic disease is intricate, since many diseases develop in years but identification of a specific dietary cause is utterly challenging. The conception of “risk factors” has been added to the public language, ever since, the landmark Framingham Heart Study which begun in 1948. This study reported for the first time in the early 1960s that cigarette smoking, high blood pressure and elevated blood cholesterol levels were predictors of one’s tendency of dying by heart disease (Weininger, 2019). Not all the people having a risk factor ultimately develop a particular disease; yet, the chances of developing the disease increases many folds when a known risk factor is present. Some of the major risk factors are diet, lack of physical activity and consumption of tobacco or alcohol; others include heredity, age and gender. Some modifiable risk factors are exposure to sunlight and other radiations, biological agents and chemical agents that may induce genetic mutations and have been correlated with increased risks of certain diseases, especially cancers (World Cancer Research Fund/American Institute for Cancer Research, 2007; Heianza and Qi, 2017).

Food cholesterol and blood cholesterol are different entities, but they are often confused. Foods of animal origin only contain dietary cholesterol it is specifically high in egg yolk and meats. Diet high in cholesterol is responsible for increasing LDL cholesterol level much more than saturated fatty acids do. Further, the response to dietary cholesterol is dependent up on person to person (Dimitriou and Dedoussis, 2012).

Cancer is the major killer after cardiovascular disease in much of the world for the adults ages 45 and older. The different types of cancers vary not only in body part and cell type affected but also in the disease, treatments and contributing factors. In migration studies, nutrition is one of the important environmental and lifestyle factors studied; however identification of particular dietary component which affects the changing rates and progression of the disease has been more mysterious. It has been estimated by many cancer organizations around the world that 30–40% of cancer cases could be prevented by following proper dietary interventions. Several types of cancer including colorectal, prostate, uterine, pancreatic, and breast cancers have also been associated with obesity (Hruby et al., 2016). A probable cause for this may be increased levels of estrogen, insulin and other related hormones that usually escort high body fat. High alcohol intake has also been implicated in the development and progression of different types of cancers, particularly of mouth, throat, liver, and esophagus (where it acts synergistically with tobacco) and possibly of breast, colon, and rectum. A confusing connection between health and food is portrayed by the fact that moderate use of alcohol may have a beneficial effect on cardiovascular disease (Meadows and Zhang, 2015).

In addition to above, the knowledge of various nutrition based diseases such as Celiac disease (caused due to allergy of wheat protein gluten), Kwashiorkar (Protein deficiency), Anemia (Iron deficiency), Stunting (Zinc deficiency) and osteoporosis (Calcium deficiency in bones) with many others are also major factors in determining consumer concerns toward healthy and targeted food products.

3.36.3.2.2 Awareness due to Various Public Health and Nutrition Based Programs

The United Nations (UN) has been continuously immersed in promoting and protecting health around the world since its inception. World Health Organization (WHO) within the UN has been leading this effort, whose constitution came into existence on April 7, 1948. This is the day when World Health Day is celebrated every year throughout the globe. In the beginning, top priorities of the WHO were destined toward fighting malaria, women’s and infant’s health, tuberculosis, venereal disease, nutrition and health problems associated with environmental pollution etc. Many of these are still on the agendas of WHO as of today, furthermore some relatively new diseases has also been included presently, like HIV/AIDS, diabetes, cancer and emerging diseases such as SARS (Severe Acute Respiratory Syndrome), Ebola or Zika virus etc. International Classification of Diseases was defined by WHO 10 1948, which has now become the international standard for explaining and reporting diseases and health conditions

Table 1 Nutrient-deficiency based diseases with symptoms and key nutrient rich food

No.	Disease	Key nutrient involved	Symptoms	Key nutrient rich food
1.	Xerophthalmia	Vitamin A	Blindness from chronic eye infections, poor growth, dryness and keratinization of epithelial tissues	Liver, fortified milk, sweet potatoes, spinach, greens, carrots, cantaloupe, apricots
2.	Rickets	Vitamin D	Weakened bones, bowed legs, other bone deformities	Fortified milk, fish oils, sun exposure
3.	Beriberi (thiamin)	Thiamin	Nerve degeneration, altered muscle coordination, cardiovascular problems	Pork, whole and enriched grains, dried beans, sunflower seeds
4.	Pellagra	Niacin	Diarrhea, skin inflammation, dementia	Mushrooms, bran, tuna, chicken, beef, peanuts, whole and enriched grains
5.	Dermatitis, microcytic hypochromic anemia	Vitamin B6	Impaired immune function, depression, confusion, and convulsions	Lean meat, sea foods, legumes, nuts
6.	Scurvy	Vitamin C	Delayed wound healing, internal bleeding, abnormal formation of bones and teeth	Citrus fruits, strawberries, broccoli
7.	Vitamin E deficiency	Vitamin E	Fragility of red blood cells (hemolysis) is seen; in the latter, where deficiency is more prolonged, neuromuscular dysfunction involving the spinal cord and retina may result in loss of reflexes, impaired balance and coordination, muscle weakness, and visual disturbances	Dry fruits, nuts, fish liver oil, polyunsaturated fatty acid rich plant oils
8.	Iron deficiency	Iron	Decreased work output, reduced growth, increased health risk in pregnancy	Meat, spinach, seafood, broccoli, peas, bran, whole-grain & enriched breads
9.	Osteoporosis	Calcium	Reduced bone mass, later in life. As bones lose density, become fragile and unable to withstand ordinary strains; the resulting fractures, particularly of the hip, may cause incapacitation and even death	Nuts, seeds, green leafy vegetables, cheese, yoghurt
10.	Goiter	Iodine	Enlarged thyroid gland, poor growth in infancy and childhood, possible mental retardation, cretinism	Iodized salt, saltwater fish
11.	Kwashiorkor	Protein-energy malnutrition	Under-weight in infancy and childhood, retarded growth, skin and bones appearance of the body, swollen belly (edema), fatal diarrhea, dry and peeling skin, hair discoloration	Clean and hygienic food made from legumes, whole-grain cereals
12.	Ketosis	Long-term carbohydrate inadequacy	Distinctive sweet odor to breath	Fruits, vegetables, legumes, whole-grain cereals
13.	Essential fatty acid deficiency	Essential fatty acid	Dry skin, hair loss, and impaired wound healing	Polyunsaturated plant oils, fatty fish, fish liver oil,

Modified from Weininger (2019) and Wardlaw and Kessel (1999).

throughout the world. For the first time, the member states of WHO have set the global goals for prevention and control of heart disease, diabetes, cancer, chronic lung disease and other non-communicable diseases in 2012. From 2007, 14 November has also been designating as World Diabetes Day by the UN General Assembly. This resolution encourages the Member States for developing their national policies for the treatment i.e., prevention and care of diabetes in line with the sustainable development of their health-care systems (Source: <http://www.un.org/en/sections/issues-depth/health/>, accessed on July 08, 2019).

WHO estimates that, intake of trans fats leads to more than 500,000 deaths of people from cardiovascular disease annually. On 14th May 2018 WHO released "REPLACE", a guide to eliminate industrially-produced *trans*-fatty acids from the global food supply. This will serve as a key to protect health and help in saving millions of lives. Industrially-produced *trans* fats are most frequently present in hardened vegetable fats, most likely as margarine and ghee, and are generally present in snack food, baked foods, and fried foods. These fats are used by manufacturers often as there is no shelf life limit of these fats. But healthier alternatives can be used without affecting taste and associated cost of food. According to WHO Director-General, Dr Tedros Adhanom Ghebreyesus, "Implementing the six strategic actions in the REPLACE package will help achieve the elimination of trans fat, and represent a major victory in the global fight against cardiovascular disease". The term REPLACE was explained as first alphabet of six targeted actions as follows;

1. **Review** industrially produced dietary sources of *trans*-fats and the landscape for stands in need of policy change.
2. **Promote** the replacement of trans fats produced by of industry with healthier fats and oils.

3. **Legislate** to banish industrially-produced trans fats.
4. **Assess** and monitor *trans*-fats measure in the food supply and swap in *trans*-fat consumption in the population.
5. **Create** awareness of the adverse health effects of consumption of *trans*-fats among policy makers, producers, suppliers, and the public.
6. **Enforce** consent of policies and regulations.

Certain high-income countries have legally imposed the limits on the amount of trans fats present in packaged food and has thus virtually eliminated industrially-produced trans fats. A few governments around the world have also carried out nationwide bans on the use of partially hydrogenated oils which is the prime source of industrially-produced *trans*-fats. Actions are also required in low- and middle-income countries, where such controls on use industrially-produced *trans*-fats are often fragile, thus ensuring health benefits for the population around the world equally.

According to WHO recommendations, the total dietary intake of *trans*-fat should be limited to less than 1% of total energy intake, which decipher to less than 2.2 g/day with a 2000-calorie diet. *Trans*-fats are subjected to increased risk of LDL-cholesterol, a well-endorsed biomarker for cardiovascular diseases, and decreases HDL-cholesterol, which carry away cholesterol from arteries and send it to the liver, that secretes it into the bile. High in *trans*-fat diets increase risks of heart disease by 21% and deaths by 28%. Furthermore, it was marked that *trans*-fat may also increase inflammation and endothelial dysfunction (Source: <http://www.who.int/news-room/detail/14-05-2018-who-plan-to-eliminate-industrially-produced-trans-fatty-acids-from-global-food-supply>).

On 17th January 2019, in the response of global nutrition challenge, an e-learning platform on Nutrition Knowledge Hub (NKH) has also been designed by WHO for building the nutrition capacity of its staff. This program targeted to structure the technical and functional capacities of related WHO staff via e-learning courses. The other prime goal of NKH is to augment the acceleration and increase of nutrition impact at the country level. The NKH offers free courses (Source: <http://www.who.int/nutrition/topics/en/>, accessed on July 03, 2019). According to [Tham et al. \(2018\)](#), there is an urgent necessity of integrated health care systems in Asia. In addition to above various health promoting and awareness programmes are being running in various parts of world (some e-links are given for detailed information) and these are also contributing toward enhancing consumer awareness for personalized nutrition.

1. European Union health program: https://ec.europa.eu/health/funding/programme_en
2. Pan-Canadian Healthy Living Strategy: <https://www.canada.ca/en/public-health/services/health-promotion.html>
3. Government of India: <https://www.nhp.gov.in/healthprogramme/national-health-programmes>

3.36.3.3 Advances in Application of Information Technology in Food Science

It is well known fact that advances in information technology has made a great impact on all corners of research and developments and food science is no exception. It has also experienced a great deal of application of information technology in various research, technical, developmental, economical and analytical aspects along with marketing preferences. Food plays the key role in regulating the various processes within the body. However, admiration has been increasing for the role of nutrition in halting the growth of various chronic diseases. Significant efforts has been continued to make for encouraging the increase of nutritional potential and quality of food sources. Food science has developed excellently by extending its boundaries to various arising techniques as "omics". As per this diversification, hardship occurs in interpretation and consolidation of complex and huge raw data types. In order to that, it is important to establish a database which is able to store and keep updating the vast biological data and resources that sustain importance for food sciences as well as for nutritional sciences. In this way, bioinformatics has become a popular tool in Foodomics. Over the last years, bioinformatics has allowed systematic analysis of large data lists and has summarized the most significant aspects by utilizing the biological knowledge accumulated in public databases ([Cifuentes, 2012](#); [Kumar and Chrdia, 2017](#)).

Bioinformatics is the use of advanced computer sciences in handling biological data, for application in gathered biological information in food science, nutritional science, clinical studies or biotechnology. Bioinformatics can be utilized to access huge data related to all genomics, proteomics and metabolomics discovered so far and to transform this data in comprehensive form to make available to respective individual, industry, company or organization; for increasing quality, taste and nutritional value of food, is to be produced. By using bioinformatics we can conclude the behavior of an organism. The GMOs and products require special shelf-life condition in food industry (as yeast) by incorporating molecular dynamic simulation. One of big achievements of bioinformatics with respect to foodomics is the prediction of the amino acid sequence and protein's 3D structure; composed of specific genes can be attained and the eventual prediction of effects or side-effect can be determined. Various organizations design nutrient data where information regarding nutritional values of different food items have been uploaded that is accessible through internet. Any individual can produce a desired diet plan by using this information in minutes. Utilization of bioinformatics methods is economic and influential in comparison to lab kits. Currently, algorithms for the integration and analysis of data have been developed to minimize the level of error ([Cifuentes, 2009, 2012](#)).

Expansion of bioinformatics is taking place at an alarming rate and emerging as an essential tool for research in life sciences by assimilating the traditional techniques with extensive amount of data generated through the fields of comparative genomics and proteomics ([Desiere et al., 2001](#)). Evaluation of allergic potential of respective proteins has been become easier by the integrating bioinformatics tools, likewise playing an important part in safety assessment of genetically modified crops also. This technique

assists by the prediction of functionality and allergenicity of various food products by estimating the amino acid sequence of their ingredient protein (Ladics et al., 2011). Comparative genomics technique via bioinformatics has been practiced significantly in many food borne pathogens that have been attraction for many sequencing and comparative genomic research projects (Mayer et al., 2011).

In addition to above, creative advertisement of targeted food products in wide publicity domains such as television, internet, mobile and media has also influenced the consumer choice toward specific foods and information technology has made great impact on personalized nutrition in this way.

3.36.3.4 Concept of Gene-Diet Interaction

Due to change in the food habits, sedentary life-style and inevitable stress, major portion of the population is suffering from the nutritional inadequacy. This irregularity in nutritional uptake becomes one of the most prominent reasons of health related disorders such as obesity, cardiovascular problems, diabetes mellitus etc. and considered as major health concern for all age groups, globally. Recent studies revealed that apart from environmental factors, the interplay of various genes is responsible for these detrimental health issues. The elaborative research on various genome wide approaches including molecular genetics analysis, linkage analysis, polymorphisms, identification of qualitative trait loci (QTL) and genetic markers helped in unraveling the mystery of multiple gene interaction which resulted in multifactorial life-threatening diseases (Helali et al., 2013; Guasch-Ferré et al., 2018). Overcome the consequences of such diseases, the study of detailed genetic basis and underlying role of genes in diseases is crucial (Ashley, 2016). In this section, we will discuss how various gene-diet interactions and genetic susceptibility can lead to complex disorders along with their possible causes and treatment.

Nutritional genomics is nascent branch of science which helps in elucidating the effect of individual's diet on their gene expression and how individual's genetic make-up responds in respect to the components of diet and their metabolism (Vyas et al., 2018). Nutrigenomics is highly significant to study the association between genetic variants and diet-related disorders, which can help in defining dietary strategies and guidelines to prevent monogenic as well as polygenic diseases.

Obesity is a multifactorial disorder which is characterize as excessive accumulation of body fat, affecting normal physiological processes of body and might give rise to other serious diseases such as cardiovascular disorder, type 2 diabetes, chronic respiratory diseases, musculoskeletal problems, hormone related cancers, large-bowel cancer and gallbladder diseases (WHO, 2003; Gadde et al., 2018). The environmental factors which cause obesity are obesogenic lifestyle, excessive calorie intake, poor physical activity which leads to imbalanced Basic Metabolic Index (BMI) (Shuldiner and Munir, 2003). Moreover, studies suggested that genetic factors also play crucial role in enhancing individual's susceptibility to obesity, more than 200 genes have been identified by genetic mapping analysis that might contribute to obesity (Speakman, 2007). Using genome-wide association studies (GWAS), obesity is characterized as polygenic as well as monogenic obesity. QTL approaches followed by position cloning on human chromosome detected several obesity prone genes such as chromosome 10p, 11q24, 16p, 18q21, 20q13, and Xq24 on various chromosomal regions. The investigation and comparison of these genes in obese and non-obese people suggested that obesity can be a polygenic trait (Chagnon et al., 2000a). Trp64Arg β 3-adrenoceptor (Walston et al., 1995) and Pro12Ala peroxisome activated Receptor γ 2 (PPAR γ 2) (Yen et al., 1997), are two genetic variants which might have minor influence on obesity phenotype. Extensive study of single genes on animal models indicated the co-relation of monogenic obesity in humans. Among several hundred genes, most studied and common obesity related genes are leptin (LEP), leptin receptor (LEPR), agouti-related peptide (AgRP), tubby gene, POMC gene (Rankinen et al., 2006). LEP gene encodes hormone leptin which is secreted by adipose tissues, it regulates the appetite and energy consumption of the body, hence significantly affect the fat mass ratio of the body (Farooqi et al., 2007). The treatment of obese mouse with mutated recombinant leptin resulted in decreased appetite, controlled body weight with normal phenotypic characters (Iwaniec et al., 2007). When the intracellular leptin signaling cascade has been studied, the structural similarity between leptin and cytokine was found and it was deduced that leptin might act by cytokine receptor. An intracellular protein, the suppressor of cytokine signaling-3 (Socs-3) which down-regulated the action of cytokine receptor, might mediates the inhibition of leptin signaling, hence causing leptin resistance (Kievit et al., 2006). The rodent leptin receptor (LEPR) gene which is similar to human LEPR encodes 1164 amino acids long protein with 22 amino acid secretory signal sequence, transmembrane and cytoplasmic domain (Bouchard, 1995). A splice-mutation in leptin receptor yielded truncated receptor without transmembrane and intracellular domains of receptor (Farooqi and O'Rahilly, 2006). Obese people with such mutation showed controlled adiposity, establishing relationship between LEPR gene signaling and obesity (Farooqi et al., 2007). POMC (Pro-opiomelanocortin) gene expression is associated with the expression of mRNA essential for active form leptin receptor and leptin hormone. Pro-hormone convertase 1 (PC-1) mediates the post-translational modification of POMC, yielding biologically active peptide. Mutation in gene encoding for PC-1 thus inhibits the cascade and found significant in controlling obesity (Chagnon et al., 2000b; Farooqi and O'Rahilly, 2006).

Several other studies based on gene-diet interactions and gene-physical activity interactions repetitively indicated the involvement of Fat mass and obesity associated (FTO, rs9960939) locus and PPARG (Pro12Ala) locus in obesity (WHO, 2003). The individuals with little or no physical activity and improper BMI showed high expression of FTO gene. When the co-relation between diet and risk of obesity was studied, it was observed that excessive consumption of fried food and sugar with sedentary lifestyle, potentially enhances obese gene expression with high adiposity. But genetic susceptibility, risk of obesity can be controlled and the effect of FTO gene can be down regulated by healthy & monitored diet, lifestyle with high to moderate physical activity (Kilpeläinen et al., 2011; Qi et al., 2012, 2014). PPARG is nuclear receptor which control number of genes and their signaling cascade, and regulate

various metabolic pathways such as adipogenesis and energy utilization. The variants with modified Pro12Ala locus showed controlled weight and obesity (Franks et al., 2007).

Cardiovascular disease (CVD) is another complex group of disorders which is characterized by dysfunctioning of heart and blood vessels, it comprises, cerebrovascular disease, coronary and periphery artery disease, congenital heart disease and heart attack (Dimitriou and Dedoussis, 2012). Along with behavioral and metabolic risk factors, genetic predisposition is also associated with CVD. After extensive GWAS, chromosome 9p21 was identified as genomic loci for coronary heart disease (O'Donnell and Nabel, 2011). Various gene-diet interactive studies concluded that controlled dietary patterns i.e. high intake of raw vegetables, fruits, nuts, green leafy vegetables and milk products with healthy life style can surpass the genetic effects of chromosome 9p21 in CVD-associated genetic variants (Do et al., 2011). MTHFR gene encodes 5–10 Methylene tetrahydrofolate reductase (MTHFR) which catalyzes the reduction of 5, 10 methylene tetrahydrofolate to 5-methyltetrahydrofolate and it is an important enzyme for folate and homocysteine metabolism (Song et al., 2018). During the study of MTHFR polymorphism, the single base substitution of cytosine by thymine causes substitution of valine by alanine, due to which decreased enzyme activity resulted in high homocysteine concentration in plasma, which is further marked by increased risk of thrombosis and thereby high cardiovascular risk (Chen et al., 2016). PPARs family (peroxisome proliferator-activated receptor) is one of the most relevant gene family studied for gene-diet interaction for CVD. PPARs are the transcription factors regulating gene expression by interacting with specific response elements (PPREs) in the promoter region Gearing et al., (1994) and control the adipocyte differentiation, fat accumulation, glucose and lipid metabolism (Latruffe and Vamecq, 1997). Two years long nutritional study with Mediterranean diet and conventional low-fat diet in large group of patients revealed that Pro12Ala polymorphism of the PPAR- γ 2 gene which is associated with high adiposity and cardiovascular risk, can be effectively subsided by following Mediterranean diet and manifested by reduced waist circumference (Razquin et al., 2009). Another apolipoprotein (APO-A and APO-E) gene family regulates the concentration of triglycerides, VLDL, HDL, LDL, lipid metabolism and thus plasma lipid concentration in the blood. The intake of PUFA along with other diet interventions reduces VLDL and triglyceride levels while enhancing HDL concentration in blood. The APO-A1 gene polymorphism study indicates the significance of APO-A variations to elucidate the atherogenic profile of the subject and could be significant in diagnosis and treatment of CVDs (Ordovas et al., 2002; Tortosa-Caparrós et al., 2017).

The Type II diabetes mellitus (T2DM) is another major disease affecting population globally and the genetic and environmental factors are closely related to obesity. GWAS showed that TCF7L2 (transcription factor 7-like 2 gene), Kir6.2 & SUR1 (pancreatic β -cell KATP channels two subunits), IRS1 (insulin receptor substrate 1), DHCR7 rs12785878 (7-dehydrocholesterol reductase) are few elaborately studied genes which causes genetic susceptibility to T2DM (Hani et al., 1998; Goldstein et al., 2000; Saxena et al., 2012). Study of TCF7L2 gene locus give insight about its significant role in T2DM, as it involved in secretion of insulin in β -cells of pancreas. Polymorphism in this gene correlated with low insulin production, hence increasing the T2DM risk. Consumption of whole grain (high fiber content) with high physical activity suggested beneficial effect on diabetes risk, assumed to be improved activity of TCF7L2 gene (Fisher et al., 2008). ATP-sensitive K^+ channels (KATP channels) of pancreatic β -cells are important to maintain insulin secretion, SNPs in ABCC8 and KCNJ11 genes, which encodes two subunits (Kir6.2 and SUR1) of KATP channels have been associated with defect in insulin secretion leading to T2DM (Hani et al., 1998; Seino, 1999; Barroso et al., 2003). PTPN1 gene encodes protein tyrosine phosphatase-1B (PTP1B) which down regulates the insulin signaling pathway by specially dephosphorylating tyrosine residues from insulin receptor kinase activation domain along with IRS1. Genetic variants of mice with defective PTPN1 gene locus showed enhanced insulin sensitivity and controlled obesity (Elchebly et al., 1999). Another study highlighted the role of vitamin-D in insulin and obesity resistance. Two years long analysis on large group of participants showed that vitamin-D metabolism-related variants of DHCR7 gene with high-protein diet might have improved insulin resistance (Qi et al., 2015a). Several other significant genes involved in gene-diet interaction have been listed in the Table 2.

Table 2: Genes involved in gene-diet interaction.

On the basis of above discussion we can say significant data available from Human genome project helps us in understanding structure, function and organization of human genes. Moreover, the advances in technology for genome analysis such as genome wide association studies, single nucleotide polymorphism, genotyping, gene marker studies and high-throughput genetic sequencing methods, made understanding and analysis of various disease related genes accessible for scientific community. The valuable data generated from all these techniques helped in identification of polygenic diseases, their prevention, treatment and cure, ultimately improving human health (Calkin and Tontonoz, 2010; Ashley, 2016; McCarthy, 2017).

3.36.3.5 Growing Consumer Concern Toward Health/Novel Foods for Better Health

Now this is the time when consumer thinks about the health, healthy living and health food even at high cost. For consumer health is in front and center to achieve that he churns out the food products that lines supermarket shelves. Now the status of health, weight, body size and shape is the area of concerned and the consumer is very much familiar with this well-known fact that specific foods can push to fulfill such wanting. This thoughtful change has been carried out by the concept of "Personalized Nutrition" basically, in order to acquire the healthy life. Consumers now also sniff out for fresh, organic and minimally processed foods which contain beneficial ingredients that helps fight against diseases and promote good health. Health attributes are now utmost substantial matter to most emerging-market respondents, who are willing to pay a premium price for health benefits, especially the younger consumers. Consumers get repelled to buy foods with artificial, color, flavors and preservatives, whereas wish to buy food manufactured from fruits and vegetables.

Table 2 Genes involved in gene-diet interaction

<i>Genetic variants</i>	<i>Outcome/Risk association</i>	<i>Study</i>
FTO rs 15558902	Insulin resistance	Zheng et al. (2015)
DHCR7 rs 12785878	Insulin resistance	Qi et al. (2015a,b)
IRS1 rs1522813, rs2943641	Insulin resistance; body weight; metabolic syndrome	Qi et al. (2011, 2013)
FTO rs9939609, rs1558902	Body composition and fat distribution; appetite	Zhang et al. (2012), Huang et al. (2014)
TCF7L2 rs12255372	Body composition; insulin resistance	Fisher et al. (2008), Mattei et al. (2012)
TCF7L2 rs7903146		
PPARG Pro12Ala	Obesity risk	Memisoglu et al. (2003)
PLIN 11482GA, 149945AT	Insulin resistance	Corella et al. (2006)
SCARB1 exon1, rs4238001	Insulin sensitivity	Perez-Martinez et al. (2005)
FTO	Obesity risk	Reddon et al. (2016)
FLJ35541	BMI	Ahmad et al. (2016)
LPL (lipoprotein lipase)	HDL-C	Ayyappa et al. (2017)
TCF7L2 and MC4R	HDL-C	Bodhini et al. (2017)
FTO rs 17817449	CVD; T2DM; obesity risk	Duicu et al. (2016)
INSIG2 rs17047757, rs7566605	Obesity risk	Malzahn et al. (2014), Kaulfers et al. (2015)
APO-A rs3135506	Obesity risk	Domínguez-Reyes et al. (2015)
ALOX-5	CVD	Mehrabian et al. (2002)
ALOX-12/15	CVD	Merched et al. (2011)
FPR2/ALX	CVD	Petri et al. (2014)
ChemR23/ERV1	CVD	Fernández (2018)
Ac2-26 (annexin A1 peptide)	CVD	Drechsler et al. (2015)

Among the most modern trends the major thrust has been for organic produce and organic ingredients present in packaged foods. According to Food Navigator (Daniells, 2018), at times, 81% of American families buy organic foods and it is estimated that the section will have grown by 14% between 2013 and 2018. So-called “Paleo diet” and “clean eating” are two next fashionable health trends that have recently emerged and the trend seems to get broaden in near future. These diets are diversified, but rely heavily on “free-from” products, even if they are dairy-free, sugar-free or gluten-free. In USA the total market of gluten-free products was estimated to grow and achieve \$2.34 billion mark by 2019 that is an increase of 140% from 2014. As per Neison Global health and wellness report (Nielsen, 2015), 49% of global respondents believed that they are over-weight and 50% were trying to lose weight. However, fortified/functional foods are fading their shine in the western world as the synthetic and processed offering, but Asia Pacific is still taking probiotic yoghurt as a hot trend. Moreover, fortification of micronutrients is the key in growing market to address malnutrition.

3.36.4 Application of “Omics” Tools and Techniques in Nutrition Science

With rapid advances and diversity in promising analytical platforms and computer based analysis, research in food science and nutrition is likely to be revolutionized by the use of “omics” applications in the near future (Alfaro and Young, 2018). The term “omics” is collectively referred to the technologies used for analysis of structure, function, and intermolecular interactions of various biomolecules in biological samples (Coughlin, 2014). These technologies are used in “high-throughput” leading to multiple measurements simultaneously and identification of global set of gene products i.e., expressed genes, proteins and metabolites in studied sample(s). The commonly used high-throughput “omics” measurements includes genomics, transcriptomics, proteomics, and metabolomics. The outcomes of these measurements are affected by the external stimuli including environmental factors (both macro and micro-environments), genetic makeup of individual, experimental conditions and nutritional status etc. Therefore, the developments in above high-throughput “omics” technologies provide numerous opportunities for understanding the effect of diet at molecular level and huge variability in responses. The technological innovation is required for enhancing the capacity and efficiency of diagnostics of various diseases, immunology, nutritional formulation in addition to determining the safety and quality of foods (Browdy et al., 2010). As revealed from literature, importance and relevance of “foodomics” or “omics” technologies in food and nutrition has got a recent attention (Herrero et al., 2012; Ibáñez et al., 2012; Castro-Puyana and Herrero, 2013; Cifuentes, 2013). A brief overview of these tools is discussed in following sections.

3.36.4.1 Genomics and Transcriptomics

After the sequencing of human genome, the genomic sequencing technology has transformed the research of biological science and this technology has now also being practiced in clinical science leading to generation of genomic data from over 60 million patients globally and is expected in healthcare in next 5 years (Birney et al., 2017). Internationally, investments of over US\$4 billion have been made by governments of more than 14 countries in recent years, for the establishments of genomic-medicine initiatives

(Manolio et al., 2015). Since 2013, the governments of at least 14 major countries have invested to address implementation barriers and transition testing from their centers of excellence to mainstream medical practice. Transcriptomics studies reveals expression status of particular gene(s) or complete set of expressed genes of an individual at a time (transcriptome) and its outcome is mainly dependent on use of technologies such as real-time-PCR and robust DNA-microarrays. In addition, RNA sequencing (RNA seq) has emerged as a robust alternative for transcriptome analysis as it is covering larger spectrum of RNAs and providing more functional information (Bodian et al., 2019). Transcriptomics analysis provides opportunities for study of mRNA expressed or changes in expression of gene(s) in experimental samples as consequences of changes in diet or other factors (Liu and Qian, 2011).

For example, transcript profiling has been extensively used to evaluate the possible effects of anthocyanins on obesity related gene expression in adipocytes (Tsuda et al., 2006), biomarker identification (Picó et al., 2019) and also for designing precise mitigation strategies especially for ready-to-eat food products (Soni et al., 2011). Several robust and nutrient-specific microRNAs (miR) as indicators of nutritional stress have been reported in plants (Scheible et al., 2011). Taking use of deficiency indicators miRNAs in plants, if found, such indicators will be extremely useful in determining the urgency of specific nutrition to consumer.

3.36.4.2 Metabolomics

The term “metabolomics” is referred to study of metabolites or small molecules present in biological samples. The complement of overall metabolites in any sample is known as its “metabolome” (Nobeli and Thornton, 2006). The outcome of this technology is mainly dependent on use of analytical technique with high separation efficiency and reproducibility i.e. GC-MS, proton nuclear magnetic resonance (NMR), HPLC-TOF-MS (along with upgraded technology UPLC-TOF-MS). These are becoming less time consuming and opened numerous opportunities of screening for metabolites in food components, body fluids and tissues *in situ* and changes therein in response to effect of diet, environment or genetic factors (Herrero et al., 2012; Lorach et al., 2012). Rimbach et al. (2008), considered metabolomics as end point of human molecular analysis. Its applications to studies for dietary interventions allows a greater understanding of effect of individual’s diet on undergoing metabolic changes, one’s health and related disorders along with relationship between genotype and phenotype. For example, metabolomics have been used in different studies for evaluating metabolite profiles as a result of consuming fiber (Johansson-Persson et al., 2013), tea (van Velzen et al., 2009), coffee (Redeuil et al., 2011), fish oils (McCombie et al., 2009), high-fat diet (Rubio-Aliaga et al., 2011) and large number of metabolic perturbations were revealed. The metabolomics approach can be used for nutritional interventions, to identify dietary biomarkers and for the development of personalized nutrition or medicine (Brennan and Hu, 2019; Collins et al., 2019; González-Peña and Brennan, 2019).

3.36.4.3 Proteomics

Traditional nutrition research was mainly concerned with supplementing nutrients for nourishment and on prevention of specific nutrient deficiencies or disorders. But recently, with the advent of -omic technologies, the aspects of nutritions have broadened and it now even investigates various health aspects of individual ingredients in diet, in view of their health promoting effects, performance optimization, and assessment of possible disease prevention. Personalized nutrition relates to all possible health benefits, prevention of the onset of disease and is analogous to personalized medicine by adapting suitable foods to individual specific needs. Modern nutrition research has build the foundation for understanding the variability in terms of preferences, requirements and responses to a diet at an individual level and may become an empirical tool for assessing personalized nutritional counseling for health maintenance and disease prevention (Kussmann, 2010). Deciphering the molecular interplay between food and health requires the use of holistic approaches so that of important health aspects must not be compromised. Recent approaches utilized for investigating an individual’s response to its diet include the use of -omics technologies viz., genomics, metabolomics and proteomics together with the systems biology approach (Hood et al., 2004; Qi, 2014). These -omics technologies integrate and analyze the data generated during dietary intervention studies along with potential effects on personalized nutrition. There is need for a comprehensive understanding of the interrelationship between nutrition and corresponding health benefits apart from the knowledge of network dynamics in the context of diseased and pre-disease states (Verma et al., 2018).

Nutriproteomics is still a nascent research area, which exploits the proteomic tools to characterize molecular and cellular changes in protein expression and their interaction with other nutrients as the bioavailability and functions of each nutrient including bioactive peptides and proteins can be influenced by the presence of other nutrients/compounds. Nutriproteomics may serve as a potential tool in personalized nutrition. Nutriproteomics may help in quantification and/or characterization of bioactive peptides and proteins derived from food apart from discovering the biomarkers for elucidating their mechanism of action and efficacy (Kussmann, 2010). Endogenously expressed human proteins and peptides may also be used as biomarkers to monitor physiological responses at an individual level. Bioactive peptides and proteins derived from food in general exert multiple responses such as growth and homeostatic regulation and can even cause adverse allergic reactions in some cases (Sauer and Luge, 2015). Proteomics is central to nutrigenomic research and describes how our genome expresses itself as a response to the diet. Proteomics in nutrition can identify and quantify bioactive proteins and peptides and also addresses their nutritional bioefficacy (Kussmann and Affolter, 2009). Application of proteomic techniques for determining food quality especially with respect to personalized nutrition is mainly done by analyzing the complete proteome or metabolome of foods (Werf et al., 2001) Proteomics approach may even be used in the post-marketing surveillance of foods derived from genetically modified crops and may serve as an important tool in near future (Kuiper et al., 2001), in identification of bioactive compounds in nutraceuticals and functional foods (Galvani et al.,

2001), apart from diagnosis and vaccine/drug development (Plowman et al., 2000). Nutriproteomics may also be potentially used in medical and nutritional research for revolutionizing biomarker and drug development, nutraceutical discovery, biological process modeling, preclinical nutrition linking diet and diseases and structuring ways to a personalized nutrition. Though several challenges such as protein dynamics, analytical complexity, cost and resolution needs to be addressed, but still the scope of application of proteomics in personalized nutrition is rapidly expanding and promising new and holistic strategies for nutritional intervention may emerge in near future (Ganesh and Hettiarachchy, 2012).

3.36.5 Future Challenges and Conclusion

Based on the facts and discussion in previous sections, it is evident that the science of precision nutrition has made great progress owing to availability of numerous research studies as proof of concept toward its effectiveness. Without any doubt, it is need of the hour to decipher the knowledge of complex gene-diet interaction, which is becoming even more complex due to developments of novel food products elsewhere. Therefore, the actual implementation of successful models is immensely important task for real time success of concept. Issues including ethics related to sharing of generated genomic data, higher variability of “omics” data in samples, lack of trend manpower for generation, analysis and handling of big data, need to be addressed.

According to Ferrocino and Coccolin (2017), only a few examples of multi-omics approaches are available in the literature and these approaches need to be implemented to obtain a better understanding of food microbial ecosystems. However, this approach also suffers from certain limitations, due to its relatively high cost and the need for specific bioinformatics and biostatistics skills for the data analysis. Additionally, the higher cost of analysis makes this investigation as unapproachable to majority of population (Puiggròs et al., 2011).

Furthermore, the complexity of the problem increases concurrently with the presence of various nutrients, with diverse chemical structures having numerous targets with distinct affinities and specificities (McCabe-Sellers et al., 2009). In the future, the fusion of Foodomics and systems biology can bring crucial information about host-microbiome interactions, nutritional-immunology, food microorganisms including pathogens resistance, farm-animal production, etc., or to completely understand the postharvest phenomena through a universal approach that connects genetic and environmental responses and identifies the fundamental biological networks.

3.36.6 Conflict of Interest

No conflict of interest is declared by authors.

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